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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 19:11:10 ; Search time 38 Seconds (without alignments) 25.320 Million cell updates/sec

US-10-047-945-1 54 Perfect score:

1 LKAMDPTPPL 10 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

1102

seq length: 0 seq length: 10 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	trypsin-modulating	lectin - potato (f	urease (EC 3.5.1.5	peptide-N4-(N-acet	major protein anti	enamelin f - bovin	T-cell receptor be	exotoxin A - Strep	collagen alpha 2(V	T-cell receptor be	metallothionein-A	alcohol dehydrogen	triacylglycerol li	hementin (EC 3.4	alpha-gliadin 4Ha	alpha-gliadin 6Ha	acid proteinase li	ATPase R1 subunit	orf 1 rara 5'-regi	Ig H chain V-D-J r	granulocyte-colony	dissimilatory sulf	vitamin D3 26-mono	probable methionin	Ig H chain V-D-J r	T-cell receptor be	. probable glucose-6	ycerc	Ig mu chain J regi
SUMMARIES	Ð	A36454	S2128B	C35389	B59272	B60274	S10783	B30572	A60108	S26508	C30572	151049	871919	PC2171	A61007	A61218	B61218	B37988	D48186	S15594	PH1633	I54017	S63491	S15850	B39517	PH1592	PT0664	S18396	PX0030	F33932
	DB	7	~	~	~	~	7	~	N	~	~	~	7	~	7	~	7	~	~	4	7	4	~	7	7	~	N	~	~	0
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de	Query Match	50.0	44.4	38.9	8	37.0	37.0	35.2	35.2	ď.	35.2	•	m	33.3	'n.	Н	31.5	σ	σ	σ	•	27.8	27.8	27.8	27.8		27.8	7	27.8	27.8
	Score	27	24	21	21	20	20	19	19	19		18	18	18	18	17	17	16	16	16	16	15	15	15	15	15	15	15	15	15
	Result No.	-	7	e	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ICL2 protein - Par	Ig heavy chain CRD	tryptophyllin, bas	endoglycosylcerami	hypothetical prote	T-cell receptor be	leucopyrokinin - M	neuropeptide calla	ribosomal protein	bradykinin - horn	orf dowstream to b	hydroxyproline-3-b	bradykinin-like pe	Thr-6 bradykinin -		ornitho-kinin - ch
871299	PT0283	A61081	B39745	S16324	PT0559	A23967	E47393	S35538	\$65433	B41983	A43065	A26744	A61057	A60579	B60246
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25.	25.5	25.	25.9	25.	25.	25.9	25.	25.	25.	25.	25.9	25.	25.9	25.	25.
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

		- yellow
		factor
		oostatic
LT 1	54	sin-modulating

trypsin-modulating oostatic factor - yellow fever mosquito
(Species Aedes aegypti (yellow fever mosquito)
(S.pacies: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
(S.Accession: A36454; A61630
(R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
A58GB J. 4, 3015-3020, 1990
A; Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
A; Reference number: A36454; MUID:90367888; PMID:2394318

A;Accession: A36454

A; Molecule type: protein A; Residues: 1-10 < BOR> A; Cross-references: UNIPROT:P19425 B; Borovesky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F. Insect Biochem. Mol. Biol. 23, 703-712, 1993 A; Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost A; Reference number: A61630; MUID:93357794; PMID:8353526 A; Accession: A61630; MUID:93357794; PMID:8353526 A; Residues: 1-10 < BO2>

A;Note: none of the amino acids is modified C;Function: A;Description: inhibits systhesis of trypsin- and chymotrypsin-like enzymes by midgut ep C;Keywords: hormone

Length 10; 2; 50.0%; Query Match Best Local Similarity

ö Gaps ö 1; Indels Score 27; DB 2 Pred. No. 58; 0; Mismatches 4; Conservative Matches

DPAPP 6 N a

q

5 DPTPP

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RESULT 2

lectin - potato (fragment)

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A; Reference number: A60274; MUID: 91099989; PMID: 1898899
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C;Keywords: enamel; phosphoprotein
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75.0%;
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Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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                                      A;Accession: B60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
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R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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C;Species: Purnus dulcis var. Sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_chann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

By Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

By Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

By Alterier, Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A; Argefarence number: A59272; MUID:98181894; PMID:9523720
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-10 <ALT->
A; Cross-references: UNIPROT:P81898
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide-NW-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain N,Alternate names: peptide N-21ycoaldase (S.5)species: Prunus dulcis var. sativa (sweet almond) C.5pecies: Prunus dulcis var. sativa (sweet almond) C.5pecies: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cipate: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C35389
C;Accession: C35389
C;Accession: C35389
C;Accession: C35389
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of capacerence number: A35389; MUID:90264298; PMID:2345135
A;Accession: C35389
A;Accession: 
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C; Date: 11-Dec_1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 2; Length 10;
Pred. No. 6.6e+02;
0; Mismatches 2; Indels
                                                                         h 44.4%; Score 24; DB 2; Length 8; Similarity 57.1%; Pred. No. 2.8e+05; 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: hydroxyproline; lectin
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity
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ASTPSPP 8
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C'Accession: $10783

Statawich, B.; Glimcher, M.J.

Bur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albuatefeesseroe number: $10780; MUID:90336641; PMID:2379503

A;Accession: $10783

A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Williams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989
Arfitle: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz
A;Reference number: A30563; MUID:89110038; PMID:2563271
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C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
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C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60108
R;Schlievert, P.M:; Gray, B.D.
Infect. Immun. 57, 1865-1867, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell receptor beta chain C region (CRTB29) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C;Accession: B30572
                                                            Gaps
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                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
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   Length 5;
Score 20; DB 2; I
Pred. No. 2.8e+05;
0; Mismatches 1;
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75.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 1;
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Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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A;Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast A;Reference number: A60108; MUID:89254013; PMID:2498210
A;Accession: A60108
A;Molecule type: protein
A;Residues: 1-9 <SCH>
A;Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNIE C;Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen alpha 2(VI) chain - bovine (fragment)
C)Species: Bos primigenius taurus (cattle)
C)Accession: 326508
R)Jander, R: Rautenberg, J: Glanville, R.W.
R)Jander, R: Rautenberg, J: Glanville, R.W.
A)Title: Brother 133, 39-46, 1983
A)Accession: 326506
A)Accession: 326506
A)Accession: 326508
A)Accession: 326508
A)Accession: S26508
A)Accession: Accession: Acce
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(230572
T-call receptor beta chain C region (CRTB49) - rat (fragment)
(5,8pecies: Rattus norvegicus (Norway rat)
C,5pecies: Rattus norvegicus (Norway rat)
C,5pecies: Rattus norvegicus (Norway rat)
C,5pecies: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C,5pacesion: C3072
R;Williams, C.B.; Gutnan, G.A.
J. Immunol. 142, 1027-1035, 1989
A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz A;Reference number: A30563; MUID:89110038; PMID:2563271
A;Reference number: A30563; MUID:89110038; PMID:2563271
A;Reference number: MID:89110038; PMID:2563271
A;Residues: mRNA
A;Residues: 1-10 < WIL->
C;Keywords: T-cell receptor
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Pred. No. 2.8e+05;
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Best Local Similarity 75.0
Matches 3; Conservative
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: IS1049 R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P. Bur. J. Blochen. 230, 344-349, 1995 A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) me A;Reference number: IS1049; MUID:95324545; PMID:7601121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Accession: S71919
B;Accession: S71919
Biochim. Biophys. Acta 1296, 41-46, 1996
B;A;Title: Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol de A;Reference number: S71919; MUID:96350418; PMID:875527
B;Accession: S71919
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Cispecies: Rhizopus niveus
Cipate: 03.Amy-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
CiAccession: PC2171
R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
A;Hitle: Publification, characterization, and crystallization of two types of lipase from A;Reference number: PC2171; MUID:94319059; PMID:7765029
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                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 cOLS>
A;Residues: 1-8 cOLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
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C; Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
C; Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 18; DB 2; Length 4; ilarity 100.0%; Pred. No. 2.8e+05; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-8 <TSU>
A;Cross-references: UNIPROT:Q7LZ46
A;Note: the source is designated Ctenopharyngodon idellus
C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 18; DB 2; Le Similarity 100.0%; Pred. No. 2.8e+05; 3; Conservative 0; Mismatches 0;
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Alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
C,Species: Haynaldia villosa, Dasypyrum villosum
C,Species: Haynaldia villosa, Dasypyrum villosum
C,Accession: A61218
R,Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D.
Blochem. Genet. 29, 207-211, 1991
B,Ochem. Golden. 207-211, 1991
B,Ochem. 207-2
hementin (EC 3.4,...) - Amazon leech (fragment)
C;Species: Haementeria ghilianii (Amazon leech)
C;Species: Haementeria ghilianii (Amazon leech)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 355-369, 1990
A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from A;Reference number: A61007; MUID:90256973; PMID:2187898
A;Accession: A61007
A;Residues: protein
A;Residues: 1-10 <SWA>
A;Cross-references: UNIPROT:Q7M3P9
C;Keywords: anticoagulant; hydrolase; saliva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.3%; Score 18; DB 2; Length 10; Best Local Similarity 50.0%; Pred. No. 2.2e+03; Matches 3; Conservative 1; Mismatches 2; Indels
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Search completed: May 26, 2005, 19:23:37 Job time : 41 secs

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haynaldia v neurospora

polyomaviru carassius c

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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MEDLINESOSCEPEUM, 11550ESCVAIY;
MEDLINESOSCEPERS FURMED-2394318;
BOZOVSKY D., Carlson D.A., Cafffin P.R., Shabanowitz J., Hunt D.F.;
"Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
enzyme blosynthesis in the midgut.";
PASEB J. 4:3015-3020(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development.
- In SEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs and grops at 56 hrs.
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MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
MEDLINE=93357794; PubMed=83556; DOI=10.1016/0965-1748(93)90044-S;
Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
Insect Biochem. Mol. Biol. 23:703-712(1993).
-I FUNCTION: Has an oostatic activity, Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
22-OCT-2004 (Rel. 45, Last annotation update)
Trypsin-modulating oostatic factor (TWOP) (OOSH).
Trypsin-modulating oostatic factor (TWOP) (OOSH).
Eddes aegypti (Yellowfever mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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YD -> DY (in TMOF(B)).
236D0A7777776DC7 CRC64;
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                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A36454; A36454.
Direct protein sequencing; Hormone.
DOMAIN 3 10 Poly-P
Q9Q0X3
Q9Q0X5
Q9Q0X5
Q9QX6
Q7LZ46
Q7M3P9
Q76MM1
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   PRELIMINARY;
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Best Local Similarity
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SEQUENCE.
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Q7M1V6;
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Compugen Ltd.
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                   GenCore version
Copyright (c) 1993 - 2005
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Q7M1V6
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Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Match Length
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seq length: 10
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Score

Result . 9 ö

Gaps

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PRISE PRUDU STANDARD; PRT; 10 AA.
P81898;
25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A small chain (EC 3.5.1.5.2) (PNGase A subunit B) (Glycopeptide N-glycosidase) (N-glycanase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borodin A.M., Danilkoyich A.V., Allikmets R.L., Rostapshov V.M., Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.; "Nucleotide sequence of the rpoB gene coding for the beta-subunit of RNA polymerase in Pseudomonas putida."; Dokl. Biochem. 302:1261-1265 (1988).
BMBL; X15849; GAA3847.1; -.
                                                                                                                                                                                                                                STRAIN=CC-2290;
MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
PF26 (Fragment)
Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                        "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
Eukaryotic Cell 2:362-379(2003).
EMBL; AY454155; AAR20844.1; -.
                                                                                                                                                                                                                                                  Kathir P., LaVoie M., Brazelton W.J., Haas N.A., Lefebvre P.A., Silflow C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Pred. No. 1.6e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
RpoB beta-subunit of RNA polymerase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1
SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;
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Pred. No. 1.6e+06;
0; Mismatches 1;
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75.0%;
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   PRELIMINARY;
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Best Local Similarity
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                                                         Lectin (Fragment).
Solamum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the deep-sea gulper eel mitochondrial genomes: largescale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
                                                                                                                                                                                                        Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R., Bolwell G.P., "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding."; Biochem. J. 283:80180: 1992).
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

44.4%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels
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Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA; 1217 MW; D99C5E75A76AA736 CRC64;
                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATPase subunit 8 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                 8 AA; 771 MW; C37775A771B5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eurypharynx pelecanoides (pelican eel).
Mitochondrion.
   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASTPSPP 8
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4 LDPSP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=ATPase 8;
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SEQUENCE
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RESULT 3 Q76MKS

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RESULT 4 Q6SP94

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Gaps

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Prunus dulcis (Almond) (Prunus amygdalus)

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4 ATAPLPP 10
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKPP 4
                                                                                                                                                                                                                                                                     Plasmid pKP31
                                                                                                                                                                                                                         Name=intIl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UF04 MOUSE
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SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
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                                                                                       Q67BK2
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UF04 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
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                                                RESULT 8
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                                                                                                                                                                    Altmann F., Paschinger K., Dalik T., Vorauer K.;
Altmann F., Paschinger K., Dalik T., Vorauer K.;
"Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A and its N-glycans.";
Bur. U. Biochem. 252:118-123(1998).
-!- CATALYTIC ACTIVITY: Hydrolygis of an N(4)-(acetyl-beta-D-glucosaminer lesidue may be further glycosylated, to yield a (substituted) N-acetyl-beta-D-glucosaminyl)asparagine residue may be further glycosylated, to yield a (substituted) N-acetyl-beta-D-glucosaminylamine and the peptide containing an aspartic residue.
-!- SUBUNIT: Heterodimer of a large and a small chain.
-!- FYFW: Is highly glycosylated and is resistant against self-
                                                                                                                                                                                                                                                                                                                                                                                                                           deglycosylation.
-!- MASS SPECTROMETRY: MW=21247; METHOD=MALDI; RANGE=1-10; NOTE=Ref.1.
PIR; B59272; B59272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
NCBI_TaxID=3755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hu L. T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T., "Morganella morganii urease: purification, characterization, and isolation of gene sequences.";
J. Bacteriol. 177:3073-3080(1990).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the urease gamma subunit family.
PIR; C35389; C35389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Morganella.
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Pred. No. 4.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 1; Length 10;
Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AA; 1171 MW; 4B313BCB077771A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA; 1149 MW; 863278CAA1E73771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct protein sequencing, Glycoprotein, Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                   SUBUNIT, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morganella morganii (Proteus morganii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct protein sequencing, Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Urease 6 kDa subunit) (Fragment).
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MEDLINE=90264298; PubMed=2345135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00739; -; 1.
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Best Local Similarity
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EPTP 4
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                                                                                                                                                        PubMed=9523720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=582;
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                                                                                                                                   SEOUENCE,
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URE3_MORMO
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Fernandez-Burriel M., Rodriguez-Quinones F., Alonso R.;

"A sull-type integron with a gene cassette for aac(6')-1b, fused in 5'
with a partially deleted gene-cassette DNA region of unknown origin.";

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY370764; AAR18813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Michter L.L., He C., Selkirk J.K.;
Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.0, its MM is: 46 kba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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01-0CT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (P46) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%; Score 21; DB 2; Lengtu ...
bred. No. 4.3e+03;
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 10 10
10 AA; 1026 MW; 9B8F5E376DC1ADC1 CRC64;
                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 766 MW; 68640AB777632700 CRC64;
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Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1:
10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 A
                                                         Created)
PRT;
                                                   25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 57.1%;
les 4; Conservative
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PRELIMINARY;
                                                                                                                                                                                                      Klebsiella pneumoniae
                                                                                                                                          Integrase (Fragment).
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Gaps

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SEQUENCE.
MEDLINE-83209648; PubMed=6852033;
Jander R., Rautenberg J., Glanville R.W.;
Jander R., Rautenberg J., Glanville R.W.;
Further characterization of the three polypeptide chains of bovine and human short-chain collagen (intima collagen).";
Eur. J. Biochem. 133:39-46(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE=Ref.1.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND MASS SPECTROMETRY.
TISSUB=Eyestalk;
Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,
Sithigorngul W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
UHA3 HUMAN STANDARD; PRT; 10 AA.

ID UHA3 HUMAN STANDARD; PRT; 10 AA.

AC P40530;

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-FEB-1995 (Rel. 41, Last annotation update)

DT 05-UTL-2004 (Rel. 44, Last annotation update)

DE Unknown protein from 2D-PAGE of heart (Spot 7513) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    freshwater prawn Macrobrachium rosenbergii.";
Comp. Biochem. Physiol. 120B:587-595(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI; RANGE=1-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
FMRFamide-like neuropeptide FLP5 (DRTPALALREF-amide).
Macrobrachium rosenbergii (Giant fresh water prawn).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Caridea;
Palaemonoidea; Palaemonidae; Macrobrachium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 1; Length 10;
Pred. No. 9.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                   Score 19; DB 2; Length 9; Pred. No. 1.68+06; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.

GO; GO:0007218; P:neuropeptide signaling pathway; TAS
Amidation; Direct protein sequencing; Neuropeptide.

MOD RES 10 TO Phenylalanine amide.

SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC771 CRC64;
                                                                                                                                                                                                                                                                 9 AA; 876 MW; 681467776867605B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.2%;
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                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Best Local Similarity
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es 3; Conserv
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                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                 PTPP 9
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SEQUENCE
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                                         Bovinae;
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Matches
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                                                                                                                                                                                                                                                                                   Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.,
"Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
insect cells.";
Shi Yan Sheng Wu Xue Bao 28:283-290(1995).
EMBL; S80660; AABSO110.1; -.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
                                                                                                                                   Rattūs sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                         01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Luteinizing hormone/chorionic gonadotropin receptor homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U57303; AAB17863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.0%; Score 20; DB 2; Length 10; 50.0%; Pred. No. 6.48+03; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA; 1182 MW; 22252E34176AB2D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 10 AA; 1129 MW; 09A5F22DC4177760 CRC64;
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Last annotation update)
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Last annotation update)
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NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 2; I
Pred. No. 6.4e+03;
0; Mismatches 1;
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 10 AA.
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01-MAR-2004 (TrEMBLrel. 26, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last seque
Collagen alpha 2(VI) chain (Fragment)
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19. Last sen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                   TISSUE=Ovary;
MEDLINE=96147985; PubMed=8571710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.0%;
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   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Chorion; Receptor.
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                                                                                                                                                                                          NCBI_TaxID=10118;
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PIPP 5
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                                                                                                                     Fragment).
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Q7M2M9 Q7M2M9

RESULT 12 Q7M2M9

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STRAIN=TYLCV-IB;
Wernecke M.B., Roye M.E, McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U84397; AAB47965.1; -.
NON TER 10 10
SEQUENCE 10 AA; 1058 MW; 25FF98B5A775A5A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                     TISSUB=Heart,
MEDLINE=95203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                             1994.";
Electrophoresis 15:1459-1465(1994).
-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown protein is: 6.8, its MW is: 47.3 kDa.
Direct protein sequencing.
NOW TER 10 10 Aa; 1049 MW; 6BBCDE41A041B76B CRC64;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                35.2%; Score 19; DB 1; Length 10; 60.0%; Pred. No. 9.5e+03; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.2%; Score 19; DB 2; Length 10; 50.0%; Pred. No. 9.5e+03; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2 protein (Fragment).
Tomato yellow leaf curl virus (TYLCV).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA.
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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1 AVEPT 5
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P90391
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Search completed: May 26, 2005, 19:22:05 Job time : 168 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model • OM protein Run on:

May 26, 2005, 18:45:04; Search time 158 Seconds (without alignments)
24.479 Million cell updates/sec

US-10-047-945-1 54

1 LKAMDPTPPL 10 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

465227 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 10 Minimum DB E Maximum DB E Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

STIMMARTES

		de			SUMMAKIES		
Result No.	Score	Query Match	Length	DB	ID	υ	g
п	54	100.0	10	~	AAW53843	Aaw53843 N	N-terminu
7	54	100.0	10	7	ABB80222		Synthetic
m	20	95.6	σ	7	ABB80227	Abb80227 Sy	Synthetic
4	43	79.6	80	۲.	ABB80228	Abb80228 S	Synthetic
Ŋ	30	55.6	9	4	AAB68473	Aab68473 M	Mutated p
9	30	55.6	80	S	ABB78481	Abb78481 Gt	Gum arabi
7	30	55.6	10	ស	ABB78478	Abb78478 Gt	Gum arabi
œ	28	51.9	6	~	AAY47988	Aay47988 It	Immunogen
0	28	51.9	6	m	AAY86825	-	Telomeras
10	28	51.9	0	ო	AAY86735	_	Telomeras
11	28	51.9	6	80	ADK07609	Adk07609 He	Hepatitis
12	28	51.9	10	N	AAR61547	Aar61547 Pe	Peptide f
13	28	51.9	10	~	AAR93336	Aar93336 Y	YES prote
14	28	51.9	10	~	AAY48003	Aay48003 Ir	Immunogen
15	28	51.9	10	œ	ADE97778		Immunogen
16	27	50.0	9	7	AAR56874	Aar56874 Oc	Oostatic
17	27	50.0	9	7	AAR63465	Aar63465 T	Trypsin M
18	27	50.0	9	7	AAR80074	Aar80074 P.	P2 analog
19	27	50.0	9	~	AAW19715	Aaw19715 D	Digestion
20	27	50.0	9	7	AAW69749	Aaw69749 D	Digestion
21	. 27	50.0	9	m	AAB37945	Aab37945 Ti	Trypsin m
22	27	50.0	9	4	AAB30661	Aab30661 T1	Trypsin m
23	27	50.0	9	9	ABP58325	Abp58325 Ti	Trypsin m
24	27	50.0	φ	7	ADC35474	-	Trypsin m
25	27	50.0	9	7	ADD10251	Add10251 Mc	Mosquito

Aar56875 Oostatic Aar63466 Trypsin M Aar80075 P3 analog Aaw19716 Digestion Aaw57946 Trypsin m Ab57946 Trypsin m Ab58326 Trypsin m Ab58326 Trypsin m Ad58475 Trypsin m Ad410252 Mosquito Aar56873 Oostatic Aar56873 Dostatic Aar80073 P4 analog Aaw45975 Pagestion Aaw4595 Pentide #	
2 AAR56875 2 AAR63466 2 AAR80075 2 AAW69706 2 AAW69750 4 AAB30662 4 AB730662 6 ABP58326 7 ADC35475 7 ADC35475 2 AAR56873 2 AAR80073 2 AAW19717 2 AAW4595	AAB30663 AAB58327 ADC35476
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ALIGNMENTS

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LINF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                    AAW53843 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-00657163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-00058387.
94US-00310340.
                                                                                                                                                                                                                                                                            N-terminus of opossum LTNF.
                                                                                                                                                                                          08-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1996;
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                                                                                                                 AAW53843;
AAMS 3843

MAWS 3843

MAWS 3843

MAWS 3843

MAWS 3848

MAWS 3848
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Lipps FW, Lipps BV; (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

WPI; 1998-271108/24.

Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.

Claim 7; Col 11; 11pp; English.

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

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Best Loca
Matches
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ID ABB
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                                                                                                                                                                                                                                                                                    The sequences given in ABB80222-28 represent lethal toxin neutralising factor (ICTP) peptides which may be used for reducing elevated levels of secum proteins selected from immunoglobulin E (ISE), insure growth factor (MCF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum ISE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythmatcosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, diabetes, autoimmune of Hodgin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva cannel using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                      ö
enake. Being short it can be synthetically prepared rather than the
current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; ElE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g.
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                      ö
                                                                                                               Length 10;
                                                                                                               Score 54; DB 2; Length 10
Pred. No. 0.033;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      ABB80222 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 3; 24pp; English.
                                                                                                                 100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2002; 2002US-00047945.
                                                                                                                                  .00.00.
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                        1 LKAMDPTPPL 10
                                                                                                                                                                                         1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic LTNF, LT-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                       to horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003060471-A2
                                                                            Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                             Query Match
Best Local S:
Matches 10;
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                                                                                                                                                                                                                                                                                    RESULT 2
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The sequences given in ABBB0222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, dations or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invesive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 198; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SiE; rheumatoid arthritis; Siogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.9
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                  ;
                                                      100.0%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80227 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lethal toxin neutralising
                                                                                              Local Similarity 100.
                                                                                                                                                                                                       1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                        LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic LTNF, LT-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TIPP/) LIPPS (LIPPS)
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Sequence 10
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                                                                    Query Match
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us-10-047-945-1.closed.rag

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), insive growth factor (NGF), insulin, myoglobin and/or adenosinase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, clabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, at disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                      Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assay of proteins from
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                         ö
                   92.6%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.6%; Score 43; DB 7; Length 8; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be assayed by a simple ELISA test, whereas an ass:
serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                        ABB80228 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                 (first entry)
                                                         Conservative
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LKAMDPTPP 9
Query Match
Best Local Similarity
''.^a 9; Conserv?
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                                                                                          1 LKAMDPTPP
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The present sequence represents a mutated portion of an integrase. The specification describes a method for targeting integration of retrotransposon of Tyl-copia group to desired location on a chromosome. The method uses a modified integrase in a retrotransposon, where the modified integrase contains a coding sequence for a peptide portion which specifically binds to protein bound to the chromosome or to particular nucleic acid sequences on chromosome. The method is useful for targeting integration of a retrotransposon of the Tyl-copia group to a desired location on a chromosome, especially into silent chromatin. The silent chromatin targeting of Ty5 is useful for tagging genes which are affected by aging and for studying oncogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Targeting integration of retrotransposon or retrovirus into silent chromatin by transforming a cell with modified integrase having a coding sequence for a peptide portion that interacts with chromatin at desired
                                                                                                                                                                                             Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
                                                                                                                                                                                                                            chromatin;
                                                                                                                                                                                                                           Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin; chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%; Score 30; DB 4; 66.7%; Pred. No. 1.8e+06 iive 2; Mismatches
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                                                                                                      AAB68473 standard; peptide; 6 AA.
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nes 4, Conserv
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LDPSPP 6
                 LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1999;
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                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                    AAB68473;
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Matches
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ABB78481
ID ABB7
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The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPs, repetitive proline-rich proteins (RRPs) and arabinoglactan-proteins (AGPs) in plants via recombinant methodologies. Also described is the expression of synthetic genes designed from repetitive peptide sequences, such as glycoproceins (including the peptide sequences of gum arabic glycoprotein (GAGP)). ABLS1730 to ABLS1849 and ABRYB401 to ABBYB544 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide having a human leukocyte antigen binding motif #2599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytocoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                    Nucleic acids and proteins useful for producing hydroxy-proline rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.6%; Score 30; DB 5; Le 100.0%; Pred. No. 2.7e+02; Itive 0; Mismatches 0;
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                                                                                                                                                                                                                                                Claim 5; Page 121; 326pp; English.
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                     12-APR-2000; 2000US-00547693.
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                                                                                                                                                                                                         glycoproteins in plants.
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                                                            (UYOH-) UNIV OHIO.
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                                                                                                    Kieliszewski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPs, repetitive proline-rich proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via recombinant methodologies. Also described is the expression of synthetic genes designed from repetitive peptide sequences, such as glycoproteins (including the peptide sequences of gum arabic glycoprotein (GAGP)).

ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used in
                                                            Plant, Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant, Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids and proteins useful for producing hydroxy-proline rich
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                   Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 100.0%; Pred. No. 1.8e+06; 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 121; 326pp; English.
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Best Local Similarity
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1 PTPPL 5
                                                                                                                                                                                                                                                                                                                                                                                                                   Kieliszewski MJ;
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Synthetic.
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                                                                                                       AGP; plant gum
                                                                                                                                           Acacia senegal
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RESULT 7 ABB78478

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Length 10; 0; Indels ŝ

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having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allale (i.e. HLA-A subtypes HLA-A21, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotocxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for influsion back into a patient. The polymucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein or peptide fragments useful in the treatment and prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a telomerase peptide of the invention, and content or and in a method for the treatment or prophylaxis of cancer. The sequences are useful in the treatment or prophylaxis of cancer especially, breast, lung, ovarian, cervical, colorectal, prostate or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telomerase; antigenic peptide; cancer; therapy; human; tumour cell; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saeterdal I;
                    specifically claimed immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 2; Length 9;
Pred. No. 1.8e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gjertsen MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moller M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY86825 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 36; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-NO000220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98NO-00003141
                                                                                                                                                                                                                                                                                                                                                                                                                                        51.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eriksen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             telomerase T lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telomerase peptide #240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-145727/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPTTPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saeboe-Larsen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200002581-A1
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saudernack G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Best Local S
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                     1ymphocytes
   melanoma, leukaemias, lymphomas, or biliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein or peptide fragments useful in the treatment and prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and can
pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or bili. tract carcinomas. They are useful for generating telomerase T lymphocy capable of recognising and destroying tumour cells in a mammal, comprising culturing T lymphocytes obtained from the mammal with the peptides. Telomerase protein is expressed only by tumour cells, hence, other body cells are not targeted or destroyed by telomerase specific cells. Note: This sequence was indexed from WO200002581, which is the first major country equivalent to NO9803141
                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase; antigenic peptide; cancer; therapy; human; tumour cel'
malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
telomerase T lymphocyte.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a telomerase peptide of the invention,
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                         Length 9;
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                                                                                                                                                                                    Score 28; DB 3; 1
Pred. No. 1.8e+06;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 3; I
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                             AAY86735 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 35; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-NO000220.
                                                                                                                                                                                      51.9%;
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                                                                                                                                                                    Query Match
Best Local Similarity 55.6%;
Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eriksen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase peptide #150.
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                                                                                                                                                                                                                                                         2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                            1 RAODPPPEL 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saeboe-Larsen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200002581-A1.
                                                                                                                                                      Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                               AAY86735;
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Matches

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antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIVI; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1; melanoma antigen-1; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AARS9496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (AAR71293). AAR61547 has an ICS0 of 0.0042 and the sequence occurs at position 2803 in the HCV LORF protein. The peptides of the invention can induce cytcoxic T tymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3 ligand; SH3 binding agent; biased phage library; recognition sequence; src SH3 domain; Paget's disease; restenosis; rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47; p67; complex; chronic myelogenous leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                    Peptide fragment (1.0507) of HCV binds HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; I
Pred. No. 5.6e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR93336 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                        93US-00027146.
93US-00073205.
93US-00159184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A, Sidney J,
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11-MAY-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CYTE-) CYTEL CORP
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DPTTPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                        04-MAR-1994;
                                                                                                                                                                                                                                                                          WO9420127-A1
                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1993;
                                                                                                                                                                                                                                                                                                                 15-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antiganic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a hepatitis C virus CTL epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
    Gapa
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                                                                                                                                                                                                                                                                                                                                   pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; epitope peptide;
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Indels
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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ص
                                                                                                                                                                                                                                                                                             Hepatitis C virus CTL epitope peptide #5439.
Mismatches
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                                                                                                                                                                           ADK07609 standard; peptide; 9 AA.
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  1;
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80.0%;
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                                                                                                                                                                                                                                                      (first entry)
5; Conservative
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                                      2 KAMDPTPPL 10
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1 RAODPPPEL 9
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                          HLA-allele; CTL.
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Gaps

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RESULT 12 AAR61547

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Southwood S;

Grey HM,

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AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1.2 or A24.1 or HLA-B or C) and induce a cytocoxic T cell response against the antigen from which the peptide is derived. Cytocoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in cancers in mammals (especially to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B cancers in mammals (especially humans) e.g. prostate cancer, hepatitis and C. AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to the peptide e.g. to produce CILs ex vivo for influsion back into a the peptide e.g. to produce CILs ex vivo for influsion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nephrotropic; neuroprocective; antiarchritic; antirheumatic; immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic; hamunosuppressive; dermatological; muscular; nephrotropic; thyromimetic; hamunosenic peptide composition; immune response, prostate cancer; hepatitis B, hepatitis C, AIDS; renal carcinoma; cervical carcinoma; lymphoma; cytomegalovirus; CMV; condlylloma acuminatum; autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis; Sjogren syndrome; scleroderma; polymyositis; dermatomyositis; arkylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid; pemphigus; glomerulonephritis; Godpasture's syndrome; autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia; human leukocyte anitgen A2.1; HLA A2.1;
                                                                                                                                                                                                                                                                       New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%; Score 28; DB 2; Length 10; 83.3%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic HLA-A2.1 binding peptide #260.
                                                                                                                                                                Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic HLA-A2.1 binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE97778 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 132; 150pp; English
                                                                                                                                                                Sidney J,
     98WO-US005039.
                                                          98WO-US005039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5, Conservative
                                                                                                             (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                  WPI; 1999-551214/46.
                                                                                                                                                                Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 DPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
     13-MAR-1998;
                                                          13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE97778;
                                                                                                                                                                  Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR93272-342 represent peptides which are SH3
[1gands/SH3 binding agents. They represent a biased phage library which
comprises six random amino acids flanking the tetrapeptide -PPIP which
comprises six random amino acids flanking the tetrapeptide -PPIP which
was identified as a recognition sequence for the src SH3 domain. These
sequences were identified using the method of the invention. The method
comprises contacting the SH3 domain with a mixture of peptides under
conditions permitting a ligand to bind to an SH3 domain to form a
complex. Any unbound peptides are removed and the complexed peptide
ligands are dissociated from the complexes. The selected peptide
such the SH3 domain are detected. The selected peptides are
enriched by re-contacting them with the SH3 domain and then candidates
which bind to the SH3 domain are detected. The isolated SH3 binding
peptides may be used in the dispossis, prevention and treatment of
conditions or diseases resulting from cellular processes mediated by an
SH3-based interaction. Such diseases include Paget's disease. Other
conditions treatable with these peptides include restences; rheumatoid
arthritis, gout and other problems in which an SH3 of neutrophil oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTD; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                     Identification of peptide(g) binding specifically to SH3 domains - for use in inhibiting interactions mediated by SH3 domains in treatment of e.g. osteoporosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%; Score 28; DB 2; Length 10; 55.6%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                 Botfield MC, Zoller MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY48003 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1; 74pp; English.
                                                                                                       95WO-US003208
                                                                                                                                                             94US-00209835
                                                                                                                                                                                      95US-00369832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 55.6
                                                                                                                                                                                                                                           (ARIA-) ARIAD PHARM INC.
                                                                                                                                                                                                                                                                                                 Brugge JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KAKRPLPPI 9
                                                                                                                                                                                                                                                                                                                                                WPI; 1995-328231/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 AA;
WO9524419-A1
                                                                                                          13-MAR-1995;
                                                                                                                                                             11-MAR-1994;
                                                                                                                                                                                      06-JAN-1995;
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                                                                                                                                                                                                                                                                                           Rickles RJ,
                                                     14-SEP-1995
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Matches

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Gaps

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The invention describes an immunogenic peptide composition comprising 9 residues including a first conserved residue at a second position from N-cerminus, and a second conserved residue at C-terminal position. The inventive peptide composition is used to elicit an immune response against a desired antigen for preventing, treating or diagnosing pathological states, e.g. prostate cancer, hepatitis B. hepatitis C, ALDS, renal carcinoma, cerrical carcinoma, lymphoma, cytomegalovirus (CMV), and condlylloma acuminatum. It is also used to treat autoimmune associated disorders, e.g. multiple sclerosis, rheumatoid arthritis, Slogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic lupus erythematosus, juvenile rheumatoid arthritis, alponentionephritis, Goodpasture's syndrome, autoimmune hemolytic anemia, Hashimoto's disease, permictous anaemia, didopathic thrombocytopenic purpura, Grave's disease, and Addison's disease. The invention defines positions within a motif enabling the selection of the peptides, which will bind efficiently to human leukcoyve anitgen (HLA) A2.1. This is the amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic peptide composition for preventing, treating or diagnosing pathological states, e.g. prostate cancer, hepatitis B and C, Acquired Immunodeficiency Syndrome, and renal carcinoma, includes conserved residues at specified positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page 25; 38pp; English.
                                                                                                                                                                    93US-00027146.
93US-00073205.
93US-00159184.
94US-00349177.
                                                                                                                                                                                                                                                                                                                                             Sette A, Sidney J;
                                                                                                                                 03-APR-2002; 2002US-00116557
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-041186/04.
                                                                                                                                                                                                                                                                  GREY/) GREY H M.
                                                                                                                                                                                                                                                                                     (SETT/) SETTE A. (SIDN/) SIDNEY J.
                                                       US2003185822-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                    05-MAR-1993;
04-JUN-1993;
29-NOV-1993;
02-DEC-1994;
                                                                                             02-OCT-2003
                   Synthetic.
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Query Match 51.9%; Score 28; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps
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S DPTPPL 10 ||||| | DPTTPL 10

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Search completed: May 26, 2005, 19:19:14 Job time : 161 secs

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May 26, 2005, 19:22:12; Search time 136 Seconds (without alignments) 25.366 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/Pcr_NEW PUB.Pep:*
2: /cgn2_6/ptodata/1/pubpaa/Pcr_NEW PUB.Pep:*
3: /cgn2_6/ptodata/1/pubpaa/Pcr_NEW PUB.Pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.Pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.Pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.Pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.Pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.Pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.Pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.Pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.Pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.Pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.Pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1462099 seqs, 344972447 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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54
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	Sequence 6, Appli	Sequence 7, Appli	168			Sequence 165, App	, et	Sequence 381, App	Sequence 20, Appl	Sequence 23, Appl	Sequence 26, Appl	Sequence 29, Appl
ID		US-10-047-945-6	US-10-047-945-7	US-10-437-708-168	US-10-418-032-168	US-10-437-708-165	US-10-418-032-165	US-08-344-824-273	US-08-344-824-381	US-09-758-128-20	US-09-758-128-23	US-09-758-128-26	US-09-758-128-29
DB	14	14	14	15	17	15	17	8	œ	6	σ	σ	0
Length	101	σ	60	80	80	10	10	9	10	ω	ω	80	œ
<pre>% Query Match Length DB 1</pre>	100.0	95.6	79.6	55.6	55.6	55.6	55.6	51.9	51.9	50.0	50.0	50.0	50.0
Score	54	20	43	30	30	30	30	28	28	27	27	27	27
Result No.	-	~	٣	4	Ŋ	9	7	80	0	10	11	12	13

Sequence 20, Appl Sequence 23, Appl Sequence 26, Appl Sequence 20, Appl Sequence 23, Appl Sequence 29, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 4159, Ap Sequence 4159, Ap Sequence 2002, Ap Sequence 2002, Ap Sequence 2002, Appl Sequence 6159, Appl Sequence 619, Appl Sequence 1620, Appl	619, 74, 619,
US-09-758-426-20 US-09-758-426-26 US-09-758-426-26 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-758-198-20 US-09-861-661-20 US-09-861-661-20 US-09-861-661-20 US-09-861-661-20 US-09-915-430-1613 US-10-224-999A-1613 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-4046 US-10-149-138-40619 US-10-224-999A-1619 US-10-224-999A-1620 US-10-224-999A-1620	10-277-292-6 -10-277-292-6 -10-280-340-7
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ALIGNMENTS

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ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
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         Sequence 1, Application US/10047945;
Publication No. US2003015755A1
GENERAL INPOWATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: LIPPS, AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: LIPPS, AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: LIPPS, AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: LIPPS, AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: LIPPS, AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: LIPPS, AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: SYNTHESIZED. OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-047-945-1
JS-10-047-945-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
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LKAMDPTPPL 10 1 LKAMDPTPPL 10

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APPLICANT: Kleliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
TITLE OF INVENTION: Glycoproteins
FILE REPERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/10/437,708
CURRENT FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US/09/547,693
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 168 Application US/10418032

Publication No. US20050074838A1
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia J.
APPLICANT: Kieliszewski, Marcia J.
TITLE OF INVENTION: Synchetic Genes for Plant Gums and Other Hydroxyproline-Rich TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-07775
CURRENT APPLICATION NUMBER: US/10/418,032
CURRENT FILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Patentin version 3.2
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (3)..(4)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline
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; DOTHER INFORMATION: The Proline at these positions is a hydroxyproline

US-10-418-032-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(1) OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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ORGANISM: Artificial Sequence
US20040009555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
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ORGANISM: Artificial/Unknown
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NAME/KEY: MISC_FEATURE
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NAME/KEY: SITE
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NAME/KEY: SITE
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US-10-418-032-168
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                                          gequence 6, Application US/10047945

Publication No. US20030157555A1

GENERAL INPORMATION:

APPLICANT: LIPPS, BNIE V.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS

TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS

CURRENT APPLICATION NUMBER: US/10/047,945

PRIOR APPLICATION NUMBER: US/10/047,945

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 6

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10047945
Publication No. US2003015755A1
Publication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APLICANT: LIPPS, BINIE V.
APLICANTON UNMBER: US/10/047,945
CURRENT APPLICATION NUMBER:
PRIOR APPLICATION UNBER:
PRIOR APPLICATION UNBER:
WINDER OF COLORS OF 
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1.3e+06;
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
LENGTH: 8
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-437-708-168
                                   -10-047-945-6
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                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (5)...(6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ... (6) ...
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LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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; Sequence 273, Application US/0834824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
    APPLICANT: SETTE, Alessandro
    APPLICANT: SIDNEY, John
    TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
    NUMBER OF SEQUENCES: 399
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: One Market Plaza, Steuart Street Tower, 20th
    STREET: Ploor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                        Query Match 55.6%; Score 30; DB 17; Length 10; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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COMPUTER: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,824

FILING DATE: 23-NOV-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/278,634

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 34,774

RELEPHONE: (415) 543-9600

TELEFAK: (415) 543-5603

INFORMATION FOR SEQ ID NO: 273:

SEQUENCE CHARACTERISTICS:

LEMBTTH: 9 amino acids

LEMBTTH: 9 amino acids
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83.3%; Pred. No. 1.3e+06;
tive 0; Mismatches 1;
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Best Local Similarity 83.3
Matches 5; Conservative
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US-08-344-824-381
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Sequence 165, Application US/10437708

Sequence 165, Application US/10437708

PUBLication No. US20040009555A1

GENERAL INFORMATION: US20040009555A1

TITLE OF INVENTION: Glycoptocins

TITLE OF INVENTION: Glycoptocins

FILE OF INVENTION: Glycoptocins

CURRENT FILING DATE: 2003-05-14

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 236

SEQ ID NO 165

LENGTH: 10
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Sequence 165, Application US/10418032
Publication No. US20050074838A1
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia J.
ATILE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-07775
CURRENT APPLICATION NUMBER: US/10/418,032
CURRENT FILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Patentin version 3.2
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CTHER INFORMATION: The Proline at these positions is a hydroxyproline. US-10-437-708-165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (3)..(3) OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 PTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
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LENGTH: 10
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Best Local Similarity 62.5
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                ; TYPE: PRT
; ORGANISM: Bovine
US-09-758-128-20
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US-09-758-128-26
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US-09-758-128-20

i Sequence 20, Application US/09758128

i Sequence 20, Application US/09758128

i Sequence 20, Application US/09758128

i GENERAL INFORMATION:
    APPLICANT: KINGSTON, David J.
    APPLICANT: GERRATY, No. US20020107187Alman L.
    APPLICANT: WESTBROOK, Simon L.
    APPLICANT: WESTBROOK, Simon L.
    APPLICANT: WESTBROOK, Simon L.
    TITLE OF INVENTION: WODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
    TITLE OF INVENTION: WOBSER: US/09/758,128
    TITLE OF INVENTION: WOBSER: US/09/758,128
    CURRENT APPLICATION NUMBER: US/09/758,128
    CURRENT PILING DATE: 1990-02-05
    PRIOR FILING DATE: 1996-05-22
    NUMBER OF SEQ ID NOS: 58
    NUMBER OF SEQ ID NOS: 58
    SOFTWARE PATENTIN VET: 2.0
    LENGTH: 8
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Sequence 381, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SETTE Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: His binding Peptides AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Floor
STREET: Floor
STREET: Gome Market Plaza, Steuart Street Tower, 20th
STREET: Floor
STREET: Book
COUNTRY: USA
COUNTRY: USA
MEDIUM TYPE: Floopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: Ploopy disk
COMPUTER: DEPROS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
ATTONREY/AGENT INFORMATION:
APPLICATION NUMBER: 13,774
FILING DATE: 21-JUL-1994
ATTONREY/AGENT INFORMATION:
TELECOWALICATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 11
TELECOWALICATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOWALICATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION
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ches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-344-824-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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US-09-758-128-23

i Sequence 23, Application US/09758128

i Sequence 23, Application US/09758128

i Patent No. US20020107187A1

i GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: WESTERROOK, Simon L.

ITLE OF INVENTION: MODULARING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

ITLE OF INVENTION: MODULARING THE ACTIVITY OF HORMONES OR THEREOF

ITLE OF INVENTION: MODULARING THE ACTIVITY OF HORMONES OR THEREOF

ITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

CURRENT FILING DATE: 105/09/758,128

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR PELING DATE: 1996-05-05

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 23

LENGTH: 8

LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WS-09-758-128-26

WS-09-758-128-26

Sequence 26, Application US/09758128

Sequence 26, Application US/09758128

Sequence 26, Application US/09758128

Sequence 26, Application US/02010118741

Sequence 26, Application US/02010118741

APPLICANT: KINGSTON, David J.

APPLICANT: KINGSTON, David J.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

CURRENT APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR PRILING DATE: 1996-02-05

PRIOR APPLICATION NUMBER: AU PN9990

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 58
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Query Match 50.0%; Score 27; DB 9; Length 8; Best Local Similarity 62.5%; Pred. No. 1.3e+06; Matches 5; Conservative 1; Mismatches 2; Indels
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Pred. No. 1.3e+06;
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RESULT 15
US-09-758-426-23
i Sequence 23. Application US/09758426
i Patent No. US20020169116A1
i GENERAL INFORMATION:
i APPLICANT: KINGSTON, David J.
i APPLICANT: GERRATY, No. US20020169116A1man L.
i TITLE OF INVENTION: No. US20020169116A1man L.
i TITLE OF INVENTION: NOULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS;
i TITLE OF INVENTION: NOULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS;
i TITLE OF INVENTION: NOUNBER: US/09/758,426
i CURRENT APPLICATION NUMBER: US/09/758,426
i CURRENT FILING DATE: 1999-02-05
i PRIOR PLING DATE: 1999-02-05
i PRIOR PLING DATE: 1999-02-05
i PRIOR PLING DATE: 1996-05-22
i NUMBER OF SEQ ID NOS: 58
i SOFTWARE: PATENT VOT: 2.0
i SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 27; DB 9; 1
62.5%; Pred. No. 1.3e+06;
tive 1; Mismatches 2
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Matches 5; Conservative
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            1 AISPTPAL 8
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1 AISPTPAL
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                                                                                                                                                                                                                         ## Sequence 20, Application US/09758426

## APPLICANT: RINGSTON, David J.

## APPLICANT: RESTRATY, No. US20020169116Alman L.

## APPLICANT: RESTRATY, No. US20020169116Alman L.

## APPLICANT: WESTBROCK, Simon L.

## TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

## TITLE OF INVENTION: WODULATING APPLICATION NUMBER: US/09/758,426

## CURRENT APPLICATION NUMBER: US/09/194,218

## PRIOR FILING DATE: 1999-02-05

## PRIOR FILING DATE: 1999-02-05

## NUMBER OF SEQ ID NOS: 58

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                                       Gaps
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Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                       3 AMDPTPPL 10
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                                                                                                                                              1 AISPTPAL 8
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1 AISPTPAL 8
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 20
LENGTH: 8
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Gaps ö

2; Indels Length 8;

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Sequence 14, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 7, Applisequence 40, Applisequence 13, Applisequence 13, Applisequence 14, Applisequence 22, Applisequence 21, Applisequence 20, Applisequence 49, Applisequence 49, Applisequence 20, Applisequence 20, Applisequence 20, Applisequence 49, Applisequence 40, Applisequence 40,

ALIGNMENTS

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; Sequence 2, Application US/08657163A; Patent No. 574449; Patent No. 574449; Patent No. 574449; GENERAL INFORMATION: FREDERICK W. LIPPS; TITLE OF INVENTION: SYNTHETIC LINES AND THEIR TITLE OF INVENTION: SYNTHETIC LINES AND THEIR TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: BINIE V. LIPPS STREAT 4509 MINOSA DR. CITY: BELLAIRE STATE: TEXAS

COUNTRY: USA

COUNTRY: USA
                     US-09-295-996B-8

US-09-295-846B-11

US-09-295-924B-7

US-09-295-924B-7

US-09-851-738B-8

US-08-855-590-40

US-08-897-556A-103

US-08-897-556A-103

US-08-816-870C-22

US-08-416-870C-22

US-08-316-870C-22

US-08-316-870C-22

US-08-316-870C-22

US-08-316-870C-22

US-08-316-870C-22

US-08-316-870C-22

US-08-316-870C-318-86

US-08-316-870C-318-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 2. SEPTEMBER 1994
CLASSIFICATION: 5.1
APPLICATION: 5.1
RIGHT DATE: 10 MS/193
ATTORNEY/AGENT INFORMATION:
AMAD: JOHN P. ASEPECTOR
ANDER: JOHN P. ASEPCTOR
ANDER: JOHN P. ASEP
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STRANDEDNESS: SINGLE
TOPOLOGY: LINBAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,199
REPERRICE/DOCKET NUMBER: FWL-1
TELECOMMUNICATION INFORMATION:
TELERHONE: 713-482-2961
TELERHONE: 713-663-7290
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SEQUENCE CHARACTERISTICS:
LENGTH: 10
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\frac{1}{2}
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 168, App
Sequence 165, App
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                                                                                                                                                                                                May 26, 2005, 19:08:54 ; Search time 41 Seconds (without alignments) 18.207 Million cell updates/sec
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Sequence 16,
Sequence 16,
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Sequence 4
Sequence 4
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-23-446B-24
US-09-547-693-168
US-09-547-693-168
US-08-468-596-2
US-08-468-596-2
US-09-295-996B-12
US-09-295-996B-12
US-09-295-924B-2
US-09-295-926-3
US-09-295-968-13
US-09-295-968-13
US-09-295-996B-13
US-09-295-996B-13
US-09-295-996B-13
US-09-551-738B-13
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US-09-295-846B-17
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US-09-295-924B-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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54
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Match Length
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                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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Maximum DB e
                                                                                                                                           OM protein
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ZIP: 32606
COMPUTEN READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
                                  55.6%; Score 30; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%; Score 30; DB 100.0%; Pred. No. 43; ative 0; Mismatches
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2421 N.W. 41st Street, Suite A-1
                                                      100.0%; Prec. ... 0; Mismatches
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Best Local Similarity الاس.
المالية Sj Conservative أ
                              Query Match 55.6
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                   6 PTPPL 10
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US-09-547-693-165
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Patent No. 6639050
GRNERAL INFORMATION:
APPLICANT: Kieliaszawski, Marcia
APPLICANT: Kieliaszawski, Marcia
TITLE OF INVENTION:
Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REPERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
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; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: mxutant peptide ; OTHER INFORMATION: sequence US-09-232-446B-24
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NAME/KEY: SITE
LOCATION: (1)...(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
NAME/KEY: SITE
NAME/KEY: SITE
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-232-446B-24

Sequence 24, Application US/09232446B

Sequence 228647

GENERAL INFORMATION:

APPLICANT: Voytas, Daniel F.

APPLICANT: Gal, Xiaowu

TITLE OF INVENTION: Transposable Element Protein that Directs DNA

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

FILE REFERENCE: 2-98
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                                                                                                  Length 10;
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                                                                                                                                                                0; Indels
                                                                                                  Score 54; DB 1;
Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION TO Specific CURRENT APPLICATION TO SPECIFIC CURRENT APPLICATION NUMBER: US/09/232,446B; CURRENT FILING DATE: 1999-01-15; PRIOR FILING DATE: 1998-01-15; NUMBER OF SEQ ID NOS: 26; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 24; LENGTH: 6; TABLE OF SECTION NOR: 24; LENGTH: 6; CONTRACT OF SECTION OF SECTION
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
                                                                                               100.0%;
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
   SYNTHETIC
                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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1 LDPSPP 6
ORIGINAL SOURCE:
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SEQ ID NO 168
LENGTH: 8
          ) US-08-657-163A-2
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Sequence 165, Application US/09547693
Fatent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kielisewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NWBER: US/99/547,693
CURRENT APPLICATION NWBER: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SSOTWARE: PatentIn version 3.0
LENGTH: 10
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                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
MAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
NAME/KEY: SITE
LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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Length 8;
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; Patent No. 5358934
; GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: Of Pests
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                     4.1e+05;
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19

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Gaps
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| Patent No. 5629196
| GENERAL INFORMATION:
| APPLICANT: Borovsky, Dov |
| TITLE OF INVENTION: Materials and Methods for Control |
| TITLE OF INVENTION: OF Pests |
| TITLE OF INVENTION: OF Pests |
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSER: David R. Saliwanchik |
| STREET: 2421 N.W. 41st Street, Suite A-1 |
| CITY: Gainesville |
| CONTRIBUTED |
| CITY: Gainesville |
| CONTRIBUTED |
|
                                                                                                                                                                                                           Length 6;
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ZUP: 32606
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,596
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/
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Pred. No. 4.1e+05;
0; Mismatches 1;
                                                                                                                                                                                                           Score 27; DB 1; I Pred. No. 4.1e+05; 0; Mismatches 1;
                                                                                                                                                                                                           50.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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STRANDEDNESS: single
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Best Local Similarity
Matches 4: Conserv
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                   ; HYPOTHETICAL: N; ANTI-SENSE: NO US-08-271-698-2
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HYPOTHETICAL: NO
HATI-SENSE: NO
US-08-468-596-2
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US-09-295-996B-12
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                                                                                                                                                                                                                                                                                                                                                                                                    8
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; Sequence 2, Application US/08271698
; Patent No. 5439821
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods for Control
; TITLE OF INVENTION: Of Pests
; CORRESPONDENCE ADDRESS:
; ADDRESSE: ADDRESSE:
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 27; DB 1; Length 6; 80.0%; Pred. No. 4.1e+05; Live 0; Mismatches 1; Indels
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CITY: Gainesville
STATE: FL
COMPUTER: USA
Z1266
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATORNEY/AGENT INFORMATION:
NAME: SA11wanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMETHER OF SEQ ID NO: 2:
REGISTRATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMETHER OF SEQ ID NO: 2:
SEQUE
APPLICATION TO STATE THIS DATE: 19921211
CLIASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 17,794
REFERENCE/DOCKET NUMBER: UF/SES-127
TELEPHONE: 904-375-8100
TELEPHONE: 904-372-5800
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: AMINO ACID
STRANDEDDESS: single
TYPE: AMINO ACID
STRANDEDDESS: single
TOPOLOGY: linear
TOPOLOGY: linear
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HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-989-290-2
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STRANDEDNESS: single
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Best Local Similarity
4; Conserve
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SEQ ID NO 2
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GENERAL INFORMATION:
APPLICANT: BOROVSKY, DOV
APPLICANT: Schlesinger, Yaagov
APPLICANT: Schlesinger, Sabine M. I.
APPLICANT: Nauwelaers, Sabine M. I.
TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests FILE REFERENCE: UF-223C1
CURRENT APPLICATION NUMBER: US/09/551,737C
CURRENT FILING DATE: 1990-04-18
PRIOR APPLICATION NUMBER: US 09/295,846
NUMBER OF SEQ ID NOS: 71
SOFTWARR: Patentin version 3.1
SEQ ID NO 15
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Sequence 15, Application US/09295846B
Sequence 15, Application US/09295846B
Sequence 15, Application US/09295846B
GENERAL INFORMATION:
TENERAL INFORMATION:
TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
TITLE OF INVENTION: 19-23
CURRENT PILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 6
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Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 4; I Pred. No. 4.1e+05; 0; Mismatches 1;
                                                             APPLICANT: BOLOVSKY, DOV
TITLE OF INVENTION: PESTICIDAL PEPTIDES
FILE REPERENCE: UF-230
CURRENT APPLICATION NUMBER: US/09/295,996B
CURRENT FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
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Patent No. 6566129
Sequence 12, Application US/09295996B
Patent No. 6413530
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: TMOF peptide US-09-295-996B-12
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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GENERAL INFORMATION:
APPLICANT: BOTOWRY, DOV
TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
FILE REFERENCE: UP-224(1)
CURRENT APPLICATION NUMBER: US/09/551,738B
CURRENT FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/296,113
PRIOR FILING DATE: 1999-04-21
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Patent No. 6593299
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Alan, Bernett
APPLICANT: Alan, Bernett
APPLICANT: Dov, Borovski
TITLE ON INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
FILE REPERENCE: 4137-120
CURRENT APPLICATION NUMBER: US/09/295, 924B
CURRENT FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 54
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                                                                                                           Score 27; DB 4; Length 6; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: TWOF peptide
US-09-551-738B-12
                               ; FEATURE;
; OTHER INFORMATION: TMOF peptide
US-09-551-737C-15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                 50.0%;
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ORGANISM: Artificial Sequence
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SOTTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 6
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Best Local Similarity 80.0°
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
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US-09-551-738B-12
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| Patent No. 5629196
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Carlson, David A. |
| TITLE OF INVENTION: Materials and Methods for Control TITLE OF INVENTION: of Pests
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 |
| CITY: Gainesville |
| STATE: FL
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SOFFWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHER: 31,794
REGISCHATION NUMBER: 31,794
REGISCHATION NUMBER: 31,794
TELEPECOMMUNICATION INFORMATION:
TELEPECOMMUNICATION INFORMATION:
TELEPEAK: 904-375-8100
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APPLICATION NUMBER: US/07/989,290
                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.0 Matches 4; Conservative
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    Gainesville
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ZIP: 32606
                                                          32606
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US-08-468-596-3
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                                                                                                                                                        Sequence 3, Application US/07989290

Patent No. 5358934

GENERAL INFORMATION:

APPLICANT: Borowsky, Dov

TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: Of Pests

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: David R. Saliwanchik

STREET: 2421 N.W. 418t Street, Suite A-1

CITY: Gainesville
  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08271698

Sequence 3, Application US/08271698

Patent No. 5439821

GENERAL INFORMATION:

APPLICANT: Borovsky, Dov

TAPLICANT: Carlson, David A.

TITLE OF INVENTION: of Pests

TITLE OF INVENTION: of Pests

CORRESPONDENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENTIN Release #1.0, Version #1.25
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 19921211
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REBERENCE/POCKET NUMBER: 31,794
TELECOMMULATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 904-372-5800
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                      5 DPTPP 9
                                                                          DPAPP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                RESULT 13
US-07-989-290-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-989-290-3
                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
Matches
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FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
REGISTRATION NUMBER: 1,794
REFERENCE/DOCKET NUMBER: 1,794
FELEPAX: 904-375-800
TELEPAX: 904-375-800
TELEPAX: 904-375-800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: peptide
TYPE: peptide
TYPOLOGY: linear
MOLECULE TYPE: peptide
MOLECULE TYPE: peptide
MOLECULE TYPE: NO
US-08-468-596-3
Query Match
Best Local Similarity 80.0%; Score 27; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Search completed: May 26, 2005, 19:22:51 Job time : 42 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein 26, 2005, 19:31:54 ; Search time 38 Seconds (without alignments) 37.980 Million cell updates/sec Run on:

US-10-047-945-2 84 Title: Perfect score:

1 LKAMDPTPPLWIKTE 15 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

2523 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 15 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*

Database

2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

ES	Description	trvotophyllin. bas	-	Fc gamma receptor	Ig H chain V-D-J r		lectin - potato (f	virotoxin - destro	thyroglobulin - ra	hypothetical 1.5K	alpha-glucosidase	Ig heavy chain C r	Ig heavy chain C r	calotropin DI - mu	light harvesting c	urease (EC 3.5.1.5	peptide-N4- (N-acet	lysyl-bradykinin -	bradykinin-potenti	protein-tyrosine k	protein QF200007 -	carboxypeptidase B	major protein anti	enamelin f - bovin	glycine reductase	52.5K protein - sp	tremerogen A-10 -	dystrophin-associa	Ig heavy chain DJ	disaggregatase - M
SUMMARIES	ID	A61081	A36454	A47628	PH1620	PD0444	S21288	A58725	I58273	B39109	B61457	G37266	D37267	PT0026	PT0037	C35389	B59272	839030	XAVIBH	C59151	PA0055	A26212	B60274	S10783	A39308	S78426	JIJGO	PN0663	PH1348	A60158
	DB		~	~	N	~	~	4	~	~	7	~	~	N	~	~	~	0	-	~	7	7	7	~	~	~	-	~	~	7
	Length	7	10	15	13	15	80	7	12	15	15	13	13	14	15	10	10	10	11	11	15	15	Ŋ	89	α 0	0	12	12	14	14
de	Query	32.1		32.1	29.8	29.8	28.6	27.4	27.4	27.4	27.4	26.2	26.2	26.2	26.2	25.0	25.0	ß	25.0		25.0	25.0	23.8	23.8	ë.	•	23.8	23.8	23.8	23.8
	Score	27	27	27	25	25	24	23	23	23	23	22	22	22	22	21	21	21	21	21	21	21	20	20			20		20	20
	Result No.	•	7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

chaperone, TCP1-re	chaperone, TCP1-re	ubiquitin thiolest	ubiquitin thiolest	T-cell receptor be	exotoxin A - Strep	collagen alpha 2(v	T-cell receptor be	complement C3b rec	TcR gamma V-J regi	cell surface glyco	H+-transporting tw	protein kinase (EC	Pax-QNR, long form	dichloromethane de	serine proteinase
833801	S33802 J	S10891	PT0093	B30572	A60108	\$26508	C30572	D45900	A49037	A40207	F33160	S12904	B56884	A60929	867918
7	N	7	~	7	~	N	~	7	~	~	7	7	~	7	7
14	14	15	15	6	o,	თ	10	11	11	13	14	14	14	15	15
23.8	23.8	23.8	23.8	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6
20	20	20	20	19	19	19	19	19	19	19	19	19	19	19	19
00	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A61081

tryptophyllin, basic - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Accession: A61081
R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
R;Montecucchi, P.C.; Vortein Res. 33, 391-395, 1989
A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containi
A;Reference number: A61081

A; Accession: A61081

A,Molecule type: protein A,Residues: 1-7 < MON > C. Comment: The biological activity of this peptide was not determined.

C; Superfamily: unassigned animal peptides C; Keywords: amidated carboxyl end; hydroxyproline; skin F; 3/ Wodified site: 4-hydroxyproline (Pro) #status experimental F; 7/ Modified site: amidated carboxyl end (Pro) #status experimental

Gaps ö Score 27; DB 2; Length 7; Pred. No. 2.8e+05; 0; Mismatches 1; Indels 32.1%; 80.0%; 32.1 Best Local Similarity 80.0 Matches 4; Conservative

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8 PPLWI 12 PPSWI 6 ઠે 셤

trypsin-modulating oostatic factor - yellow fever mosquito C;Species: Aedes aegypti (yellow fever mosquito) C;Bate: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

A; Molecule type: protein A; Residues: 1-10 < BOR>

A,Cross-references: UNIPROT:P19425
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
A;Hatle: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost A;Reference number: A61630; MUID:93357794; PMID:8353526

A; Accession: A61630

A,Molecule type: protein A,Residues: 1-10 <802> A,Note: none of the amino acids is modified C,Function:

A; Description: inhibits systhesis of trypsin- and chymotrypsin-like enzymes by midgut ep

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Gaps

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Length 15;

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lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: 521288
R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P. A.Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizatio A;Reference number: 521288; MUD:92272683; PMID:1590771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virotoxin - destroying angel
C;Species: Amanita virosa (destroying angel)
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A58725
R;Faulstich, H; Buku, A; Bodenmueller, H; Wieland, T.
Bjochemistry 19, 334-343, 1980
A;Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A;Reference number: A58725; WUID:6893271; PMID:6893271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: may be involved in defence mechanism of the plant C;Keywords: hydroxyproline; lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%; Score 24; DB 2; Length 8; ilarity 57.1%; Pred. No. 2.8e+05; Conservative 1; Mismatches 2; Indels
                                                                                                                             Score 25; DB 2; I
Pred. No. 5.8e+02;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-8 <MLi>A,Cross-references: UNIPROT:Q7M1V6
A,Experimental source: var. Ulster Sceptre
C,Function:
                                                                                                                             29.8%;
ilarity 36.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
                                                                                                                                                                                                                                                                    2 KAMDPTPPLWI 12
                                                                                                                                                                                                                                                                                                         | :|| |::
2 KELDPVQKLFV 12
                              A; Residues: 1-15 < KAW>
C; Keywords: mitochondrion
   A; Molecule type: protein
                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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2 ASTPSPP 8
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A5872
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PH1620
IG Heain V-D-J region (clone B-less 40) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1620
C;Accession: PH1620
C;Arcession: D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Accession: PH1620
A;Molecule type: DNA
A;Residues: L13 < LNA
A;Residues: L13 < LNA
A;Residues: L13 < LNA
A;Residues: L13 < LNA
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Accession: A-R-628
R; Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Capel, P.J.A.
J. Exp. Med. 172, 19-25, 1990
J. Exp. Med. 199
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
C;Accession: PD0444
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998
A;Description: Proteome analysis of mouse brain.
A;Reference number: PD0441
A;Reference number: BD0444
A;Accession: PD0444
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
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0
                                                            32.1%; Score 27; DB 2; Length 10; 80.0%; Pred. No. 1.8e+02; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 27; DB 2; Length 15; 50.0%; Pred. No. 2.8e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%; Score 25; DB 2; Length 13; 80.0%; Pred. No. 5e+02;
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                                                                                                                                                                                                                                                                                                                                                        RESULT 3
A47628
Fc gamma receptor II (CD32) - human (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.1
Best Local Similarity 50.0
Matches 4, Conservative
                                                                                                                                4; Conservative
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Matches 4; Conservative
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                                                                                           Best Local Similarity
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                                                                                                                                                                                             S DPTPP 9
                                                                                                                                                                                                                                                   2 DPAPP 6
C; Keywords: hormone
                                                                Query Match
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27.4%; Score 23; DB 4; Length 7; 50.0%; Pred. No. 2.8e+05; ative 1; Mismatches 2; Indels
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C, Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

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Gaps

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Ig heavy chain C region (Py2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: G37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Fitle: Heavy and light chain variable region sequences and antibody properties of anti A;Reference number: A38740; MUID:91177923; PMID:1706720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: D37267.
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti A;Reference number: A38740; MUID:91177923; PMID:1706720
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Phytochemistry 26, 633-636, 1987
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotro
A;Reference number: PT0026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PT0026
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                                         Length 15;
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                                                                                                    Indels
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                                      27.4%; Score 23; DB 2; Le
100.0%; Pred. No. 1.2e+03;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.2%; Score.22; DB 2; L6 100.0%; Pred. No. 1.5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  j heavy chain C region (Py69) - mouse (fragment)
Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                   Query Match 27.4°
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <RUF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <RUF>
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B39109
hypothetical 1.5K protein - hepatitis C virus
hypothetical 1.5K protein - hepatitis C virus
hypothetical 1.5K protein 2
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Accession: B39109; J01585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identificati
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
Liyroglobulin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 158273
R;Musti, A.M.; Ursini, V.M.; Avvedimento, E.V.; Zimarino, V.; Di Lauro, R.
Nucleic Acids Res. 15, 8149-8166, 1987
A;Title: A cell type specific factor recognizes the rat thyroglobulin promoter.
A;Reference number: 158273; MulD:88040446; PMID:3671079
A;Accession: 158273
A;Accession: 158273
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Retainer: DNA
A;Residues: 1.12 cRES
A;Cross-references: UNIPROT:Q63579; EMBL:X06162; NID:g57368; PIDN:CAA29519.1; PID:g57369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: not compared with conceptual translation
A, Molecule type: mRNA
A, Residues: 1-15 < HANN-
A, Cross-references: GB158406
R, Rumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A, Title: Cloning and sequencing of the structural region and expression of putative core A, Reference number: JQ1584; MUID:92300349; PMID:1318944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Tetrahymena pyriformis
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C;Accession: B61457
R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purificatic
A;Accession: B61457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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B61457
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
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Pred. No. 9.6e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.
                                                                                                                                                                                                                                                                                                                                                                                                          27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 3; Conservative
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les 4; Conservative
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A; Residues: 1-15 <BAN>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LWIKT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PTPPL 10
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Gaps

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Gaps

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RESULT 15
C35389
C35389
Cycaese EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
Cycaese EC 3.5.1.5) 6K chain - Morganella morganii
Cybate: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C3538
C;Accession: C3538
R;Mu Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of ge
A;Accession: C35389
A;Reference number: A35389; MUD:90264298; PMID:2345135
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-10 < HUA>
A;Residues: 1-10 < HUA>
A;Residues: 1-10 < HUA>
A;Cycaerences: UNIPROT:P17339
C;Keywords: hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               light harvesting complex chain III/b, photosystem I - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: PT0037; PS0205
C;Accession: PT0037; PS0205
A;Reference number: PS0189
A;Accession: PT0037
A;Acce
                                                                                                                                                                                                                                                                                                                        Gaps
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C;Comment: This enzyme is classified as a plant cysteine protease.
C;Keywords: pyroglutamic acid
F;I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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                                                                                                                                                                                                     Query Match 26.2%; Score 22; DB 2; Length 14; Best Local Similarity 50.0%; Pred. No. 1.7e+03; Matches 3; Conservative 1; Mismatches 2; Indels
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PT0037
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Search completed: May 26, 2005, 19:41:22 Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 19:23:42 ; Search time 165 Seconds (without alignments) 46.553 Million cell updates/sec

US-10-047-945-2 84 1 LKAMDPTPPLWIKTE 15 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

6622

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P83455 pachymedusa		homod	homod	Q6x7v1 canis famil	Q8kz86 acinetobact	P80941 lymantria d	_	Q9ten3 anas gracil	solar	Q6se52 drosophila	Q76mk5 eurypharynx			P12509 human immun	P12511 human immun	Q8hr43 clivia mini		Q8jdm3 human immun	human i		maripa	Q8mb39 wilsonia hu		Q8mb77 odonellia h	Q8mb79 aniseia arg	Q8mb97 merremia pe	Q8mbel ipomoea alb		calotrop	O9t2d9 Rolanim tub
SUMMARIES	TPFY PACDA	TMOF AEDAE	Q96Q <u>P</u> 2	Q9UCR1	Q6X7V1	Q8KZ86	ECDE LYMDI	Q9TEN1	Q9TEN3	Q7M1V6	Q6SE52	Q76MK5	Q8IVG8	Q63579	TAT HV1W2	TAT_HV1Z8	Q8HR43	Q8JDM0	Ф8-дрмз	Q8JDM7	Q8MAZ1	Q8MAZ3	Q8MB39 .	Q8MB58	Q8MB77	Q8MB79	Q8MB97	Q8MBE1	Q43174	CAL1_CALGI	091269
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& Query Match	32.1	32.1	32.1	31.0	29.8	29.8	29.8	29.8	29.8	28.6	28.6	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.2
Score	27	27	27	26	25	25	25	25	25	24	24	23	23	23	23	23	23	23	23	23	22	22	22	22	22	22	22	22	22	22	22
Result No.	1	7	m	4	Ŋ	9	7	σ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q7mlvl oryza sativ Q988r4 gossypium h P82096 litoria rub Q9h126 homo sapien G6sp94 chlamydomon Q9p139 pseudomonas Q9p131 periodomonas Q9pr21 oncorhynchu P81898 prunus dulc P17339 morganella Q67bk2 klebsiella Q67bk2 klebsiella Q677896 oreochomina Q77896 oreochomina Q77896 oreochomina	
Q7M1V1 Q958R4 E101_LITRU Q9135 Q65P94 Q65P94 Q69133 Q99R14 BRK_ONCMY BNAS_BNUDU URE3_MORMO Q67BK2 Q77896 Q771896	
22 22 25 25 25 25 25 25 25 25 25 25 25 2	

ALIGNMENTS

TWOF AEDAE

TWOF AEDAE

TO TMOF AEDAE

STANDARD; PRT; 10 AA.

C P19425;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE TYPPSin-modulating oostatic factor (TMOF) (OOSH).

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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MEDINE-22929740; PubMed-12890727;
Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.;
"Isolation and expression analysis of the canine insulin-like factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                               MEDLINE=92129337; PubMed=1733949;
MEDLINE=92129337; PubMed=1733949;
Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
Schiffmann E., Liotta L.A.
"Identification, purification, and partial sequence analysis of
autotaxin, a novel motility-stimulating protein.";
autotaxin, a sovel motility-stimulating protein.";
NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                         11 AA; 1171 MW; 2723615AA0437737 CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Insulin-like factor 3 (Fragment).
                                                                                               Last annotation update
                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             31.0%; Score 26; DB 2; L6
100.0%; Pred. No. 2.3e+03;
tive 0; Mismatches 0;
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                     11 AA.
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01-OCT-2002 (TrEMBLrel. 22, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                         Created)
                     PRT;
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                                                       01-MAY_2000 (TrEMBLrel. 13, 01-MAY_2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, AUTOTAXIN (Fragment)
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NON TER 12 12
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                   PRELIMINARY;
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                                                                                                                                     Homo sapiens (Human)
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Q8KZ86;
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                                                                                           MEDLINE-90367888; PubMed=2394318;
Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
"Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
enzyme biosynthesis in the midgut.";
FASEB J. 4:3015-3020(1990).
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MEDLINES22643823; PubMed=12757776; DOI=10.1016/S0049-3848(03)00147-6;
Hube F., Reverdiau P., Iochmann S., Cherpi-Antar C., Gruel Y.;
"Characterization and functional analysis of TFPI-2 gene promoter in a human choricocardinoma cell line.";
Thromb. Res. 109:207-215(2003).

EMBL; AY044097; AAK72693.1.
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs and stops at 56 hrs.
PIR; A36454; A36454.
                                                                                                                                                                                                                                               MEDLINE=93357794; PubMed=835526, DOI=10.1016/0965-1748(93)90044-S; Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.; Mass spectrometry and characterization of Aedes aegypti trypsin modulating oostatic factor (TMOF) and its analogs."; Insect Biochem. Mol. Biol. 23:703-712(1993).

-!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis in the midgut which indirectly reduces the vicallogenin concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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Pred. No. 2.1e+03;
0; Mismatches 2; Indels
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YD -> DY (in TMOF (B)).
236D0A7777776DC7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Tissue factor pathway inhibitor-2 (Fragment).
Homo sapiens (Human).
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Pred. No. 1.5e+03;
0; Mismatches 1;
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                                                                                                                                                                                                                                 STRAIN-Vero beach; TISSUE=Ovary;
                                                                           STRAIN=Vero beach; TISSUE=Ovary;
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5; Conservative
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                   NCBI_TaxID=7159
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EMBL; AF173494; AAD51052.1; -.
GO; GO:0005739; C:mitochondrion; IEA
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Anas gracilis (Grey teal).
Mitochondrion.
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Best Local Similarity 66.
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    Mitochondrion.
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                                                                                                                                                  MEDLINE-22270987; PubMed=12384388; Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin B., Monti-Bragadin C., Lavenia A., Dolzani L.; Monti-Bragadin C., Lavenia A., Dolzani L.; Monti-Bragadin C., Lavenia A., Dolzani L.; Molecular characterization of integrons in epidemiologically unrelated clinical isolates of Acinetobacter baumannii from Italian hospitals reveals a limited Ddversity of gene cassette arrays."; Antimicrob. Agents Chemother. 46:3665-3668 (2002).

BMBL; AJ313334; CAC85941.1; -.
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-!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of larve and pupae.
Direct protein sequencing.
SEQUENCE 13 AA, 1357 MW; 1841B4CA3275SP764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=97387807; PubMed=9243792;
DOI=10.1002/(SICI)1520-6327(1997)36:1<37::AID-ARCH4>3.3.CO;2-3;
Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
Bell R.A.;
                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
ATPase 8 (Fragment).
Anas castanea (Chestnut teal).
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15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15-JUL-2004 (Rel. 44, Last annotation update)
Lymantria dispar (Gypsy moth).
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Best Local Similarity 66.'",
Best Local 4; Conservative
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Best Local Similarity 62.50,
Best Local Similarity 62.50,
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Name=intIl;
Acinetobacter baumannii.
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                                                                                                                                    SEQUENCE FROM N.A.
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AIDPNP 7
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                                                                                         NCBI_TaxID=470;
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P80941;
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Q9TEN1
ID Q9TE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
NCBI_TaxID=45630;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Anseriformes, Anatidae, Anas.
NCBI_TaxID=45631;
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Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
                                                                                     SEQUENCE FROM N.A.
Kennedy M., Spencer H.G.;
"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
Auk 117:154-163(2000).
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"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
Auk 117:154-163(2000).
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Pred. No. 4.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                         Score 25; DB 2; Length 14;
Pred. No. 4.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                     Mitochondrion.

NON TER 1 1 SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
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NON TER 1 1 SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
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Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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063579;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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MEDLINE=90089395; PubMed=2597675;
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Best Local Similarity 60.v-
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[2]
SEQUENCE FROM N.A.
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4 LDPSP 8
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Q63579
ID Q6357
AC Q6357
DT 01-NO
DT 01-NO
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PubMed=14762063; DOT=10.1101/gr.1329204;
Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
"Patterns of evolutionary constraints in intronic and intergenic DNA of Drosophila.";
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MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
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                    "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding."; Biochem. J. 281:813-821(1992). PIR; S21288; $21288.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7240;
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Pred. No. 6.1e+03;
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                                                                                                                                                                                                                                                    57.1%; Score 24; DB 2; Length 8; 57.1%; Pred. No. 1.6e+06; ative 1; Mismatches 2; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                            8 AA; 771 MW; C37775A771B5BDDA CRC64;
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EMBL; AY459549; AAR23007.1; -.
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                                                                                                                                                                                                                                                                                  larity 57.1%;
Conservative
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Best Local Similarity 80.0°
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SEQUENCE
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SEQUENCE
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Q6SE52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Low density lipoprotein receptor related protein 1 (Lipoprotein receptor-related protein) (Fragment).
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Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, ABO46487; BAB87160.1; GO; GO:0005739; C:mitochondrion; IEA. Mitochondrion. 10 SEQÜENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 6.2e+03;
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Biochim. Biophys. Acta 1009:229-236(1989).
EMBL; Y18524; CAD57169.1;
GO; GO:0004872; F:receptor activity; IEA.
Lipoprotein; Receptor.
NON TER. 11 11
SEQUENCE 11 AA; 1221 MW; 373D041E272737
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MEDLINE=86235450; PubMed=3012778;
Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS.";
Science 232:1548-1553(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trans-activating responsive sequence (TAR) RNA element and activates transcription initiation and/or elongation from the LTR
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Rat thyroglobulin gene (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NEBI_TAXID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Binds cyclin II (By similarity).
SUBCELLULAR LOCATION: Nuclear; nucleolar.
SUBCELLULAR LOCATION: Nuclear; nucleolar.
SUBCELLULAR SEQUENTION: SUBURIT, WMM21, WMM21, WMM21, WMM21, WMM21, WMM31, MM31, MM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 2; Length 12;
Pred. No. 7.5e+03;
1; Mismatches 1; Indels
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HIV; M12507; TAT$WMJ2.
Activator; AIDS; Nuclear protein; RNA-binding;
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Last annotation update)
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01-OCT-1989 (Rel. 12,
05-JUL-2004 (Rel. 44,
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P12509;
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SEQUENCE
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27.4%; Score 23; DB 1; Length 14;

Query Match

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 80.0%; Pred. No. 8.8e+03;
iive 0; Mismatches 1; Indels
            4; Conservative
Best Local Similarity
Matches 4; Conserv
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Search completed: May 26, 2005, 19:40:36 Job time : 168 secs

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Abr12924 Ado64358 Abr33902 Abr33902 Abr1270 Abr1260 Abr12204 Abr12234 Abr12234 Ado72483 Ado72536 Ado72536 Ado72664 Ado72664 Ado72664 Ado72664 Ado72664 Ado72664

Human Human Human

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

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Result

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The present sequence is from the N terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal peptide from lethal toxin neutralising factor.
                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                               ABR33382
ABR12770
ABR12756
ABR1261
ABR12601
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ABR12046
ABR120333
AD072363
AD072664
AD0726670
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AD0665216
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 Didelphis virginiana
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20-MAR-1997
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36.487 Million cell updates/sec
                                                                                                                May 26, 2005, 19:22:57 ; Search time 159 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 15 AA;

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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                          ABB80223 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                        14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                    14-JAN-2002; 2002US-00047945.
                                                                                (first entry)
                                                                                                             Synthetic LTNF, LT-15
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(LIPP/) LIPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                              LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorxhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 84; DB 2; Length 15; 100.0%; Pred. No. 2.1e-06; ive 0; Mismatches 0; Indels
           Length 15;
                                       Indels
           100.0%; Score 84; DB 2; I 100.0%; Pred. No. 2.1e-06;
                                        0; Mismatches
                                                                                                                                                                   AAW53841 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00058387.
                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-00657163
                                                                 1 LKAMDPTPPLWIKTE 15
                                                                                    N-terminus of opossum LINF.
                                                                                                                                                                                                                         (first entry)
        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                    Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-271108/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1993;
22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                              US5744449-A.
                                                                                                                                                                                                                         08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1998.
                                                                                                                                                                                             AAW53841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                   RESULT 2
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e.9

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IGE), nerve growth factor (NGF), insulin, myoglobin and/or adenoined edaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, albetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, atthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, con Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immensionent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva con be centrifuged immediately, whereas blood collection (for serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed as a part of the proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test.
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Claim 3; Page 3; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.0%; F
Matches 15; Conservative 0;
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ABB80225

RESULT

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Gaps ö

1 LKAMDPTPPLWIKTE 15

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LKAMDPTPPLWIKTE

toxin neutralising factor; LTNF; serum protein; immunoglobulin E;

Synthetic LTNF, LT-11

Lethal

06-NOV-2003

14-JAN-2003; 2003WO-US001044. 14-JAN-2002; 2002US-00047945

WO2003060471-A2

24-JUL-2003.

saliva; ELISA.

Synthetic.

Lipps BV, Lipps FW; WPI; 2003-636703/60.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

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IGE; nerve growth factor, NGF; insulin; myoglobin; adenosine deaminase; bbb; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                               Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
  The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTME) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MGF), insulin, myoglobin and/or adenosibase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an arti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins
                                                                                                           Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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100.0%; Pre
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 ABB80225 standard; peptide; 12
                                                                                                                                                                                                                                                                                                 14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                             14-JAN-2002; 2002US-00047945
                                                      (first entry)
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Best Local Similarity 100...
Best Local 21 Conservative
                                                                                   Synthetic LINF, LT-12
                                                                                                                                                                                                                                                                                                                                                                                                  Lipps BV, Lipps FW;
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                                                                                                                                                                                    saliva; ELISA
                                                       06-NOV-2003
                                                                                                                                                                                                                                                                      24-JUL-2003
                                                                                                                                                                                                                Synthetic.
                             ABB80225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient.
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e.g.

Claim 7; Page 4; 24pp; English.

patient.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosinse (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invesive when compared to blood collection of the serum. Saliva can be centrifuged immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                                                                                                           clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW53843 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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Gaps

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0; Indels

Mismatches

ABB80226 standard; peptide; 11 AA.

ABB80226

ABB80226 ID ABB8 XX AC ABB8 RESULT 5

1 LKAMDPTPPLWI 12

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e.g.

us-10-047-945-2.closed.rag

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNP) peptides which may be used for reducing elevated levels of factor (LTNP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IGE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In carticular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, at diagnosing and triorimmune disease (e.g. erythematosus (SLEB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva ample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from the serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                Assaying a human endogenous protein (e.g. 1gE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.078; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80227 standard; peptide; 9 AA.
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                                                                                                                          14-JAN-2003; 2003WO-US001044
                                                                                                                                                                      14-JAN-2002; 2002US-00047945
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                                                                                                                                                                                                                                                                                                   Lipps BV, Lipps FW;
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                                                                                                                                                                                                                       (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                          WO2003060471-A2.
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                                                                        24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                         LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy, anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
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Pred. No. 0.078;
0; Mismatches 0; Indels
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100.0%; Pred
0; M
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                                                                                                                          histamine reaction treatment
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94US-00310340
                                                                                                                                                                                                                                                                                                                          96US-00657163
N-terminus of opossum LINF
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1 LKAMDPTPPL 10
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                                                                                                                                                                   Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-271108/24
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            10-MAY-1993;
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                                                                                                                                                                                                                       US5744449-A.
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Gaps

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WO2003060471-A2.

saliva; ELISA

Synthetic.

saliva; ELISA

ABB80222;

RESULT 7

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Synthetic

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14-JAN-2002; 2002US-00047945.
                                                                         Lipps BV, Lipps FW;
                                                                                              WPI; 2003-636703/60
                                  (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                                                                                                 The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma. C diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Relier's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by perotein may be monitored by assaying a human endogenous protein by c performing an enzyme dimmunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection of the protein and protein an entitinged immediately, whereas blood requires
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                                                                                                                                                                            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                  clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B, IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA, sathma; diabetes; autoimmune disease; systemic lupus erythematosus; BLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; 3raves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.5%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80228 standard; peptide; 8 AA.
                                                                                                                                                                                                                             Claim 7; Page 4; 24pp; English.
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                       14-JAN-2003; 2003WO-US001044.
                                               14-JAN-2002; 2002US-00047945
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Best Local Similarity 100.00
Bernea 9; Conservative
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                                                                                                             Lipps BV, Lipps FW;
                                                                                                                                      WPI; 2003-636703/60.
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                                                                        LIPPS B V.
LIPPS F W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      saliva; ELISA
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24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80228;
                                                                                                                                                                                                      patient.
                                                                                     (LIPP/)
                                                                        (ripp/)
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gB), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (a.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva callection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires
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                              e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ng time before centrifugation to separate serum. Saliva proteins assayed by a simple ELISA test, whereas an assay of proteins fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cancer-related protein 156P1D4 HLA peptide #856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serum requires a more complicated sandwich type ELISA
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                              Claim 7; Page 4; 24pp; English.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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Best Local Similarity
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                                                                                                 patient.
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Claim 13; Page 232; 1021pp; English.
                                                                                                                                                                                             Local Similarity
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1 MDPSVPIWI
                                                                                                                                            from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200283921-A2.
                                                                                                                                                                Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                    Query Match
                                                                                                                                                                                                          Matches
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                                                                                                                            The present invention relates to novel human cancer-related genes and proteins (ABZ79120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                     New composition comprising a substance that modulates the structure of proteins and polymucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a substance that modulates the structure of proteins and polymucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
                                                                                                                                                                                                                                                                                                                   Gaps
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  Ge W, Hubert RS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; vaccine; cancer; immune response; HLA;
                                                                                                                                                                                                                                                                                              Score 41; DB 6; Length 9;
Pred. No. 1.8e+06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer-related protein 156P1D4 HLA peptide #252.
Faris M,
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            Morrison RK, Raitano AB;
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                                                                                                          Claim 13; Page 238; 1021pp; English.
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  ΡΜ,
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                                                               48.84;
 Challita-Eid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human leukocyte antigen
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Best Local Similarity
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1 MDPSVPIWI
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                                                                                                                                                                                                                                                                       Sequence 9 AA;
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Morrison K, N
Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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            Morrison K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR12017;
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                       proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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present invention relates to novel human cancer-related genes and
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Pred. No. 1.8e+06;
3; Mismatches 1;
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25-APR-2001; 2001US-0286630P
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WO200283921-A2.
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                       present
example
                                                                                                                                                                                        Gaps
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as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The sequence is a human leukocyte antigen (HLA) peptide, used in an
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Pred. No. 9;
2; Mismatches 1; Indels
                                                                                                                                                                                      1; Indels
                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer-related protein 156P1D4 HLA peptide #978.
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                                                                                                                                             Score 41; DB 6; I. Pred. No. 1.8e+06; 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morrison RK, Raitano AB;
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                                                                                                                                                                                                                                                                                                                                                                              ABR12743 standard; peptide; 10 AA.
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                                                                                                                                                                                        5;
                                                                                                                                        48.8%; £ milarity 66.7%; E Conservative 2;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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MDPSVPIWI 9
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Matches 6; Conserv
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                                                                 from the invention
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                                                                                                     Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                     ABR12743;
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers or the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic genes. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.8%; Score 41; DB 6;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jakobovits A, Challita-Eid PM, Faris
Morrison K, Morrison RK, Raltano AB;
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                                                                                                                                                                                                             ABR11875 standard, peptide; 10 AA.
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25-APR-2001; 2001US-0286630P.
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful for proteins approbes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and poptides are useful as therapeutic and alagnostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                                                                     Human, cytostatic, vaccine, cancer; immune response; HLA; human leukocyte antigen.
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Pred. No. 9;
2; Mismatches 1; Indels
                                                                     Human cancer-related protein 156P1D4 HLA peptide #356.
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Morrison K, Morrison RK, Raitano AB;
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                                                                                                                                                                                                                                                                                                    10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                             Homo sapiens.
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Sequence 4, Appli
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Maximum DB
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Sequence 6, Applisequence 252, App Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 10, Appl Sequence 160, App Sequence 160, App Sequence 24, Appl Sequence 24, Appl Sequence 192, App Sequence 192, App Sequence 192, App Sequence 25, App Sequence 25, App Sequence 168, App Sequence 165, App Sequence 228, App Sequence 21, App Sequence 228, Ap
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US-10-437-708-21
US-10-437-708-22
US-10-468-370-502

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US-10-468-496-456

US-10-185-815-6

US-10-116-275-527

US-10-116-275-527

US-10-275-27

US-10-275-27

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US-10-275-27

US-10-275-27

US-10-418-019-96

US-10-437-708-160

US-10-437-708-198

US-10-437-708-198

US-10-437-708-198

US-10-437-708-198

US-10-437-708-198

US-10-418-032-192

US-09-932-613-192

US-09-932-613-192

US-09-932-613-192

US-10-418-032-168

US-10-418-032-168

US-10-418-032-168

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ALIGNMENTS

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ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
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                                                                           APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: ULGED IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0;
                Sequence 2, Application US/10047945; Publication No. US20030157555A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: SYNTHESIZED. OTHER INFORMATION: US 5,576,297.
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LENGTH: 15
TYBE: PR
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
JS-10-047-945-2
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Sequence 501, App

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Publication No. US20030157555A1
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LENGTH: 9
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                                              Sequence 4, Application US/10047945
Fublication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIP
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Publication No. US20030157555A1

GENERAL INFORMATION:

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR INMUNOGLOBULIN E

TITLE OF INVENTION: (195) IMPLICATED DISORDERS

TITLE OF INVENTION: (195) IMPLICATED DISORDERS

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT APPLICATION NUMBER: 2002-01-14

PRIOR APPLICATION NUMBER:

PRIOR PRILING DATE:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

LENGTH: 11
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US-10-047-945-1
; Sequence 1, Application US/10047945
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Matches 12; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-047-945-5
                                  US-10-047-945-4
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LOCATION:
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APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (198) IMPLICATED DISORDERS

FILE REFERENCE: FWLPATOISUS

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT FILING DATE:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 1

LENGTH: 10
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APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
FILE REPERENCE: FWLAPATOLSUS
CURRENT APPLICATION NUMBER: US/10/047,945
FRIDR APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE:
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Pred. No. 1.3e+06;
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100.0%; Pred. No. ...
0; Mismatches
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/10047945; Publication No. US20030157555A1; GENERAL INFORMATION:
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LOCATION:
OTHER INFORMATION: SYNTHESIZED.
OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Synthetic.
US-10-047-945-6
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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GENERAL INFORMATION:
APPLICANT RATH, MATTHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                   Corresponds to fragment 1-8 of 2 above.
APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: LIPPS IMPLICATED DISORDERS

FILE REFERENCE: FWLPATOISUS

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT FILING DATE: 2002-01-14

PRIOR PILING DATE:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

LENGTH: 8

LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

REDION TYPE: F10ppy Disk, 3.50 inch, 1.44MB Storage MEDIUM TYPE: F10ppy Disk, 3.50 inch, 1.44MB Storage COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MS WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-Aug-2004
CLASSIFICATION: CURROWN>
PRIOR APPLICATION NUMBER: 08/182,248
FILING DATE: 14-DAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%; Score 43; DB 14; L
100.0%; Pred. No. 1.3e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION WIMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 COlorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 52, Application US/10930300 Publication No. US20050014138A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
; OTHER INFORMATION: Synthetic.
US-10-047-945-7
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match .
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-930-300-52
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                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                    PEATURE
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                                                 Gaps
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                                                                                                                                                                                                                                                                                                            APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PRPTIDES AND METHODS OF TITLE OF INVENTION: SH3 BINDING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 15;
                                            1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
Score 38; DB 17;
Pred. No. 1.3e+06;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.0%; Score 37; DB 66.7%; Pred. No. 99; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR PAPLICATION:
PRIOR PAPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                          US-10-161-791-444
; Sequence 444, Application US/10161791
; Publication No. US2030186863A1
; GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Sequence 239, Application US/10286457 , Publication No. US20030166004A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 790-9090
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown;
MOLECULE TYPE: peptide
US-10-161-791-444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KAMDPTPPL 10
                                                                                           S DPTPPLW 11
                                                                                                                                     1 DPTMPLW 7
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STATE: New York
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## APPLICANT: Corixa Corporation

### APPLICANT: Corixa Corporation

| JITLE OF INVENTION: Gempositions and Methods for the Detection, Diagnosis and Therapy
| TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
| TITLE REFERENCE: 014058-01440208|
| TITLE REFERENCE: 014058-01440208|
| TITLE REFERENCE: 01608-01440208|
| CURRENT APPLICATION HUMBER: US 60/186,126
| PRIOR APPLICATION NUMBER: US 60/186,126
| PRIOR PRILING DATE: 2000-03-01
| PRIOR PELLON NUMBER: US 60/200,545
| PRIOR FILING DATE: 2000-04-28
| PRIOR PELLON NUMBER: US 60/200,779
| PRIOR FILING DATE: 2000-04-28
| PRIOR PELLON NUMBER: US 60/200,999
| PRIOR PELLON NUMBER: US 60/200,909
| PRIOR PELLON NUMBER: US 60/200,900
| PRIOR PELLON NUMBER: US 60/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Marnion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Composition and Methods for the Detection, Diagnosis and Therapy,
TITLE OF INVENTION: Use Composition
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-0135210S
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Ly1484 short WHC HLA A2 class I binding peptide US-10-057-475B-10923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 15;
Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10923, Application US/10154884B
; Publication No. US20040005561A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PPLWIKT 14
|||| :|
3 PPLWNRT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-154-884B-10923
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Publication No. US20040181039A1

GENERAL INFORMATION:

### APPLICANT: Krah, Eugene

APPLICANT: Alyappa, Ashok

APPLICANT: Lawton, Canine Immunoglobulin Variable Domains, Caninized Antibodies, and

TITLE OF INVENTION: for Making and Using Them

TITLE OF INVENTION: for Making and Using Them

TITLE OF INVENTION 1000 12-20

TITLE OF INVENTION NUMBER: US/10/327,598

CURRENT APPLICATION NUMBER: US 60/344,874

PRIOR APPLICATION NUMBER: 2001-12-21

NUMBER OF SEQ ID NOS: 1139

SOFTWARE: PATENTING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 1139

SEQ ID NO 735

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based ) OTHER INFORMATION: ability to selectively bind to endothelial cells US-10-286-457-239
             APPLICANT: JENO GYURIS et al.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REFERENCE: GFCI-P01-178
CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT FILING DATE: 2002-11-01
PRIOR PPLIAGO DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SEQ ID NO 239
LENGTH: 12
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
40.5%; Score 34; DB 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 1
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algace, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Ajun
APPLICANT: Ordonez, Madia
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: canis familiaris; US-10-327-598-735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 PPLWIKTE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PPTWLOTO 10
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1 QSFDPTPP 8
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US-10-057-475B-10923
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US-10-327-598-735
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PRIOR FILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-154-8848-10923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%; Score 33; DB 15; Length 9; 71.4%; Pred. No. 1.3e+06; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 501, Application US/10468370

Publication No. US20040082039A1

GENERAL INFORMATION:
APPLICANT: Garr, Francis J.
APPLICANT: Garr, Francis J.
APPLICANT: Garter, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
APPLICANT: Walliams, Stephen
APPLICANT: Watkins, John
APPLICANT: APPLICANT
APPLICANT: Watkins, John
APPLICANT: Watk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: MHC class II binding epitope US-10-468-370-501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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3 PPLWNRT 9
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US-10-468-370-501
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4 TSPTWLKT 11

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US-10-468-496-457
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Markins, John
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Way, Jofffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REPERENCE: MRR-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-18
PRIOR PILING DATE: 2001-02-18
SROFTHERS FARESEQ FOR WINDOWS VERSION 4.0
SEQ ID NOS: 689
SOFTWARE: FastSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: MHC class II binding epitope US-10-468-370-502
Sequence 502, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-03-15
APPLICATION WINGBER: 01107012.5
ALLING DATE: 2001-03-20
APPLICATION NUMBER: 01106899.6
                                                                                                                                                                               Carr, Francis J.
Jones, Tim
Carter, Graham
Hamilton, Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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; PRIOR FILING DATE: 2001-03-20; NUMBER OF SEQ ID NOS: 2036; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 457; LENGTH: 13 TYPE: PRT; OVERANTSM: Artificial Sequence; FEATURE: FEATURE: GOTHER INFORMATION: MHC class II binding epitope US-10-468-496-457
                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 26, 2005, 19:53:55 Job time: 159 sec8
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Sequence 1, Appli
Sequence 2, Appli
Sequence 444, App
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                                                                              May 26, 2005, 19:32:43; Search time 43 Seconds (without alignments) 26.040 Million cell updates/sec
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/cgn2 6/ptodata/1/iaa/5B COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B COMB.pep:*
/cgn2 6/ptodata/1/iaa/PTUS COMB.pep:*
/cgn2 6/ptodata/1/iaa/PTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-657-163A-1

US-08-602-999A-444

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US-08-362-43A-31

US-08-362-877-31

US-08-652-877-31

US-08-652-877-31

US-08-652-877-31

US-08-652-877-31

US-08-602-999A-252

US-09-268-992-70

US-09-268-992-70

US-09-547-691-19

US-09-547-691-19

US-09-547-693-24

US-09-547-693-168

US-09-547-693-168
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US-09-995-804B-4
US-09-119-507B-21
US-09-119-507B-22
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                                                                                                                                                                                                                                                   513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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84
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Match Length DB
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29 30 35.7 13 4 US-00-130-05-23 Sequence 23, Appl 20 35.7 13 4 US-00-130-256-23 Sequence 23, Appl 20 35.7 13 4 US-00-247-693-23 Sequence 23, Appl 20 35.7 13 4 US-00-247-693-23 Sequence 23, Appl 20 35.7 13 4 US-00-247-693-23 Sequence 13, Appl 20 35.7 13 4 US-00-247-693-23 Sequence 14, Appl 20 35.7 13 4 US-00-247-693-23 Sequence 14, Appl 20 35.7 13 4 US-00-247-693-23 Sequence 14, Appl 20 35.7 13 4 US-00-247-192-14 Sequence 14, Appl 20 35.7 13 4 US-00-245-192-14 Sequence 14, Appl 20 34.5 12 US-00-240-192-14 Sequence 14, Appl 20 20 US-192-14 Sequence 14, Appl 20 US-192-14 Sequence 14, Appl 20 US-192
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE:
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Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unery Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches n. τπόλη
                                                                                                                                                                                                             PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: AUTH-SONAEVENON
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BINDE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER: TEXABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/MINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: CLASSIFICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
                                        HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
NAMEDLATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                 PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWI
FELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
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TELEFAX: 713-663-7290
TELEX:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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TYPE: ... MAIN ORDER
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TOPOLOGY ILLIERE
MOLECULE TYPE: LINERA
MOLECULE TYPE: NOTE THE NOTE
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Gaps

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44.0%; Score 37; DB 3; Length 15; 66.7%; Pred. No. 19; 1; Indels tive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: 1SOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indela
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COUNTRY: U.S.A.
ZTATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE: US/09/500,124
FILING DATE: 16-FEB-1996
ATFORMEY/AGBAT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,972
REGISTRATION NUMBER: 18,972
REJERPAN: CALAI PUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEPRAN: (212) 790-9090
TELEPAN: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 444, Application US/09500124; Patent No. 6432920 GENERAL INFORMATION: GENERAL TREORATION: Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
    LENGTH: 15 amino acids
TYPR: amino acid
TYPR: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-500-124-444
                                                                                                                                                                                                                                  2 KAMDPTPPL 10
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APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OUILLAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: EVMLKES, Dana M.
APPLICANT: RIDER, James B.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSBE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.3%; Score 54; DB 1; Length 10;
100.0%; Pred. No. 0.031;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: N. J. S. A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEAEMIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/602,999A
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REPRENCE/DOCKET NUMBER: FWL-PAT-US-011
TELEPHONE: 713-482-2961
TELEPHONE: 713-663-7290
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 444, Application US/08602999A Patent No. 6184205
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-909
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPL 10
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RESULT 8
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                                 Sequence 31, Application US/08336343A
Patent No. 567144
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Franke
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/08652877

Patent No. 6187548

GENERAL INFORMATION:
APPLICANT: Alerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Morray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: 30,742
REGISTRATION STATE AND ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.1%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
US-08-336-343A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-336-343A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-652-877-31
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Gaps
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APPLICANT: Jublin, Claes
APPLICANT: Task, Lars
APPLICANT: Annualey, Gareg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Morse, Clarence C.
APPLICANT: Mirray, Edward M.
APPLICANT: Hislm, Goran
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Martin Savitzky
STREET: ROAD-POULENC ROPER INC., 500 Arcola Rd.;
STREET: 3C43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 11;
80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                              CLASSTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: SAVIEKY, MARTÍN
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/OCKET NUMBER: 3155E-US
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEFHONE: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32;
Pred. No.
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-476-515A-31
; Sequence 31, Application US/08476515A
Patent No. 6239270
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: PA

STATE: PA

COUNTRY: USA

ZIP: 19426-0107

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compag PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE: internal US-08-652-877-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collegeville
PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KPMPPRPPL 11
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TOPOLOGY: 11
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Gaps ö

3; Indels

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APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCES 467
CORRESPONDENCES: Abonue of the Americas ATREET: 1155 Avenue of the Americas CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-ZIA.
ZIP: 10036-ZIA.
ZIP: 10036-ZIA.
ZIP: TODDY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 3; Length 12; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                    REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-5090
TELEFAX: (212) 869-9741/8864
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lealie
REGISTRATION NUMBER: 18/872
REFERENCE/DOCKET NUMBER: 1101-202
TELECHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-500-124-252

Sequence 252, Application US/09500124

Parent No. 643220

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.1%;
Best Local Similarity 66.7%;
Matches 6; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                   MOLECTLE TYPE: peptide US-08-602-999A-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: peptide
US-09-500-124-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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APPLICANT: SPARKS, Andrew B.
APPLICANT: TKAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: 47
CORRESPONDENCE ADDRESS: 67
CORRESPONDENCE ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.1%; Score 32; DB 3; Length 11; 66.7%; Pred. No. 80; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATPORNEY/AGENT INFORMATION:
ATPORNEY/AGENT INFORMATION:
TELEPHONE: 610-454-3806
TELEPHONE: 610-454-3806
TELEPARX: 610-454-3806
TELEPHONE: 610-454-3806
TELEPHONE: 610-454-3806
TELEPHONE: 610-454-3806
TELEPHONE: G10-454-3806
TELEPH
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FILING DATE: 16-FEB-1996
TORNEV A A CONTROL OF 135
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Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-602-999A-252
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; ORGANISM: Mus musculus US-09-845-583A-13
; ORGANISM: Homo sapiens
US-09-657-474-70
                                                                                                                                                            7 TPPLW 11
                                                                                                                                                                                   |||:|
7 TPPIW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14
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JETRICANT: Chen, H.

JAPLICANT: Chen, H.

JAPLICANT: Chen, H.

JAPLICANT: Chen, H.

JILLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS

JETLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS

JETLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS

JETLE OF INVENTION: UNMBER: 08/09/657,474

CURRENT FILING DATE: 1999-03-16

PRIOR PELING DATE: 1999-03-16

PRIOR PELING DATE: 1999-01-28

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-03-16

NUMBER: OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 70

LENGTH: 14
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                            Sequence 70, Application US/09268992
Batent No. 6342351
GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
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Score 32; DB 4; Length 12;
Pred. No. 88;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1998-10-28
EARLIER FILING DATE: 1998-10-28
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-06-05
SARLIER FILING DATE: 1998-06-05
SARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 70
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 70, Application US/09657474 Patent No. 6399762
  38.1%;
                                             6; Conservative
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                                                                                       2 KAMDPIPPL 10
                                                                                                                                  4 KPMPPRPPL 12
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Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 4; Conserv
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7 TPPIW 11
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US-09-657-474-70
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APPLICATION MATCH 
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LOCATION: (9)..(10)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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OTHER INFORMATION: Synthetic
NAME/KEY: SITE
LOCATION: (3)...(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (7)...(7)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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                                    Length 14;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burgeson, Robert
APPLICANT: Brunken, William Joseph
APPLICANT: Champliaud, Marie-France
APPLICANT: Hunter, Dale
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
FILE REFERENCE: 10287-0556001
CURRENT APPLICATION NUMBER: US 60/200,863
PRIOR APPLICATION NUMBER: US 60/200,863
PRIOR APPLICATION NUMBER: US 60/200,863
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 13
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 4;
Pred. No. 1e+02;
1; Mismatches
                                    Score 32; DB 3;
Pred. No. 1e+02;
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-845-583A-13
; Sequence 13, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
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; Sequence 160, Application US/09547693
; Patent No. 6639050
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                                         38.1%;
80.0%;
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ORGANISM: Artificial/Unknown
Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.1
Best Local Similarity 50.0
Matches 5; Conservative
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US-09-232-446B-11

i Sequence 11, Application US/09232446B

j Patent No. 6226647

i GENERAL INFORMATION:
    APPLICANT: VOYTES, Daniel F.
    APPLICANT: VOYTES, Daniel F.
    APPLICANT: Gai, Xiaowu

    TITLE OF INVENTION: Integration to Specific Chromosomal Sites
    TITLE OF INVENTION: Integration to Specific Chromosomal Sites
    CURRENT APPLICATION NUMBER: US/09/232,446B
    CURRENT PILIOS DATE: 1999-01-15
    PRIOR APPLICATION NUMBER: US 60/071,383
    PRIOR PILIOS DATE: 1998-01-15
    NUMBER OF SEQ ID NOS: 26
    SOFTWARE: PatentIN Ver. 2.0
    SEQ ID NO 11
                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: mxutant peptide; OTHER INFORMATION: sequence
US-09-232-446B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
; NAME/KEY: SITE

; DCOATION: (14)..(14)

; OTHER INFORMATION: The Proline at this position is a hydroxyproline.

US-09-547-693-160
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                                                                                                                           Query Match 38.1%; Score 32; DB 4; Length 14; Best Local Similarity 62.5%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.9%; Score 31; DB 3; Length 13; Best Local Similarity 57.1%; Pred. No. 1.4e+02; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 26, 2005, 19:42:09 Job time : 44 Becs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                            3 AMDPTPPL 10
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4 SLTPTPPL 11
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 19:51:16; Search time 38 Seconds (without alignments) 12.660 Million cell updates/sec

US-10-047-945-3 24

1 LKAMD 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

206 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		* Ouery			SUMMARIES	
No.	Score	Match	Length	BG	DI	Description
1	11	45.8	4	7	151049	metallothionein-A
7	11	45.8	2	7	A32516	cholecystokinin-5
m	11	45.8	2	7	B31836	20K protein - Rick
4	o	37.5	4	7	A48360	gamma subunit of P
Ŋ	σ	37.5	4	~	PL0146	·O
9	σ		4	N	JQ1273	neuropeptide Antho
7	σ	٠	S	~	B41225	copper resistance
ω		37.5	5	7	PT0624	
σ	σ	37.5	S	N	PT0651	T-cell receptor be
10	ω	33.3	ß	7	S55237	zinc-binding prote
11	7	29.5	٣	m	S13894	histidinol dehydro
12	7	29.5	4	~	A61300	22K superhelical D
13	7	29.5	4	7	I40870	phospholipase C (E
14	7	29.5	4	0	T46627	hypothetical prote
12	7	29.5	4	0	E44823	•
16	7	29.5	4	~	I57745	D-mannonate hydrol
11	7	29.5	4	N	I40804	endoglucanase F -
18	9	25.0	М	m	PT0578	T-cell receptor be
13	9	25.0	4	7	S18401	thyroglobulin - do
50	9	25.0	4	7	A41890	protein D - Escher
21	9	25.0	4	7	S43014	hypothetical prote
22	9	25.0	4	7	D41654	hypothetical prote
23	9	25.0	4	7	B53284	r
24	9	25.0	4	~	847552	ubiquitin - rat
52	9	25.0	4	~	A26209	protein-glutamine
56	9	25.0	4	~	140697	biotin A - Citroba
	9	25.0	4	7	A35779	neuropeptide Antho
28	9	25.0	4	~	A32480	achatin-I - giant
53	9	25.0	4	~	PT0271	Ig heavy chain CRD

T-cell receptor be T-cell receptor be	peptidyl-dipeptida URF2 protein - Xan major protein anti	major protein anti endo-1,4-beta-xyla angiotensin-conver	photosystem I 10.4 neuropeptide - sea Ig heavy chain CRD	Ig heavy chain CRD Ig heavy chain CRD T-cell receptor be	T-cell receptor be T-cell receptor be
PT0696 PT0711	JN0860 S70154 B60274	D60274 S70615 P00009	PQ0689 A60803 PT0267	PT0281 PT0308 PT0596	PT0513 PT0729
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99	66	ωω ω	6 6 6	φφφ	6 6
30	3 3 3 3 4 3 2	35 36 37	38 39 40	4 4 4 4 2 4 3 6	4. 4. 5.

ALIGNMENTS

RESULT 1		
I51049		
metallothionein-A - rainbow trout (fragment)		
C; Species: Oncorhynchus mykiss (rainbow trout)		
C;Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text change 21-Jul-2000	Jul-2000	
C;Accession: I51049		
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.		
Eur. J. Biochem. 230, 344-349, 1995		
A; Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) me.	ncorhyncus myki	ss) me
A; Reference number: 151049; MUID: 95324545; PMID: 7601121	•	
A;Accession: I51049		
A;Status: preliminary; translated from GB/EMBL/DDBJ		
A; Molecule type: DNA		
A; Residues: 1-4 <ols></ols>		
A; Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328	:g4379328	
Query Match 45.8%; Score 11; DB 2; Length 4;		
Best Local Similarity 100.0%; Pred. No. 2.8e+05;		

Gaps ö Indels ö 0; Mismatches 2; Conservative Matches

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RESULT 2

cholecystokinin-5 - dog
Cholecystokinin-5 - dog
Cholecystokinin-5 - dog
Cholecystokinin-5 - dog
Cholecystokinin lupus familiaris (dog)
Chace: Series Canis lupus familiaris (dog)
Chacession: 342516
R;Shively, J; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A,Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intess
A,Reference number: A32516; MUID:87153871; PMID:3826354

A; Molecule type: protein
A;Residues: 1-5 < SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystol C;Superfamily: gastrin
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Similarity 100.0%; Pred. No. 2.8e+05; 2; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 2; Conserval 4 MD 5 ઠે

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0; Gaps

0; Indels

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C;Species: Anthopleura elegantissima
C;Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Datession: JQ1273
R;Nothacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
A;Title: Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropep
A;Reference number: JQ1273; MUID:92028852; PMID:1681803
A;Accession: JQ1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: The carboxyl-terminal amide probably arises from cleavage of a following glyc C;Keywords: amidated carboxyl end; neuropeptide; phenyllactylation F;1/Modified site: L-3-phenyllactic acid (Phe) #status experimental F;4/Modified site: amidated carboxyl end (Ala) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
('Species: Pseudomonas syringae pv. tomato
('Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
('Accession: B41225
R;Cha, J.S.; Cooksey, D.A.
R;Cha, J.S.; Cooksey, D.A.
A;Citle: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: B41225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C;Species: Mus musculus (house mouse)
C;Bate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0624
R;Feeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                neuropeptide Antho-KAamide - sea anemone (Anthopleura elegantissima)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.5%; Score 9; DB 2; Len 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: newborn thymus, strain BALB/c C, Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-4 <NOT>
A;Cross-references: UNIPROT:P58705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translation not shown
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Best Local Similarity 100.
Matches 2; Conservative
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A, Molecule type: protein
A, Residues: 1-5 < CHA>
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2 KA 3
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                        C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C;Keywords: oxidoreductase
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C,Species: Pseudomonas carboxydohydrogena
C,Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gradus subunit of Protein A - Methylosinus trichosporium (fragment)
C;Species: Methylosinus trichosporium
C;Species: Methylosinus trichosporium
C;Species: Methylosinus trichosporium
C;Species: Methylosinus trichosporium
C;Species: Jo.Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A48360
R;Cardy, D.L; Laidler, V.; Salmond, G.P.; Murrell, J.C.
A;Tch. Attorobiol. 156, 477-483, 1991
A;Ttle: The methane monocxygenase gene cluster of Methylosinus trichosporium: cloning & A;Contents: OBB
A;Accession: A48360
A;Accessi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.8%; Score 11; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 0; Mismatches 0; Indels
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Tue May 31

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22K superhelical DNA-binding protein - Escherichia coli (fragment)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61300
B;Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
J; Biochem. 92, 1059-1068, 1982
A;Title: Purification and characterization of a protein from Escherichia coli which form A;Reference number: A61300; MUID:83082696; PMID:6294066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000 C;Accession: 140870 R;TOyonaga, T.; Mateushita, O.; Katayama, S.; Minami, J.; Okabe, A. Microbiol. Immunol. 36, 603-613, 1992 A;Title: Role of the upstream region containing an intrinsic DNA curvature in the negati A;Reference number: 140870; MUID:92396045; PMID:1522810 A;Accession: 140870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T46627

R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.

submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
X,Residues: 1-4 <XIS>
C;Comment: This protein resembles some of the histone-like protein of bacteria in amino
C;Keywords: DNA binding; monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417
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                                                                                                0; Indels
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                                                Length 3;
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                                             Score 7; DB 3; Lostred. No. 2.8e+05; 1; Mismatches 0
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A;Molecule type: DNA
A;Residues: 1-4 <RES>
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C,Keywords: phosphoric diester hydrolase
C; Keywords: dimer; NAD; oxidoreductase
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                                                29.2%;
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Best Local Similarity 50.0%;
Matches 1; Conservative
                                                                                                1; Conservative
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
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C.Species: Zea may8 (maize)
C.Species: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C.Accession: S55237
R.Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
B.Acchen, J. 307, 267-272, 1995
A.Title: Expression and characterization of maize ZBP14, a member of a new family of zin A.Reference number: S55237; MUID:95234046; PMID:7717986
                                                                                                                                                                                                                                                                                                                                                                                                      J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A.Ritle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A.Recession: PT0651
A.Status: translation not shown
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-5 < PEE>
A.Experimental source: day 4 postnatal thymus, strain BALB/c
C.Keywords: T-cell receptor
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histodinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
histodinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: $13894
R;Nagal, A.; Scheldegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: $13894; MUID:91112783; PMID:1989490
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                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0651
S;Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
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                                                                      0; Indels
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                    Score 9; DB 2; Length 5; Pred. No. 2.8e+05; 2; Mismatches 0; Indel
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50.0%; Pred. No. 2.8e+05;
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A,Residues: 1-3 <NAG>
A,Experimental source: var. capitata
                    37.5%;
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Matches 2; Conservative
                                                                      1; Conservative
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                    Query Match
Best Local Similarity
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SLD 5
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Whaternate names: Superprotein SNAP-25 peptide 1 - rabbit (fragment)
NyAlternate names: Superprotein peptide 1
NyAlternate names: Superprotein peptide 1
NyAlternate names: Superprotein peptide 1
Sipedaes: OryColagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: E44823
N;Licewy, A.; Liu, W.S.; Baltinger, C.; Willard, M.B.
N. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein)
A;Reference number: A44823, MUD:92044785; PMID:1941090
A;Residues: 1-4 <LUES
A;Molecule type: protein
A;Residues: 1-4 <LUES
A;Molecule type: protein
A;Residues: 1-4 <LUES
A;Molecule type: protein
A;Residues: Late <LUES
A;Molecule type: protein
A;Residues: Late <LUES
A;Molecule type: protein
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking
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A;Reference number: 223105
A;Accession: T46627
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Nolccule type: mRNA
A;Residues: 1-4 <CHA>
A;Residues: 1-4 <CHA>
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings
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Search completed: May 26, 2005, 20:00:40 Job time : 40 secs

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-1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
-1- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
-1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; PL0146; PL0146.
2Pe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes
carboxydotrophic bacteria";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carb
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Antho-Kaamide.
Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2)
dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 4 AA; 420 MW; 6DD33DD6F000000 CRC64;
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Pred. No. 1.6e+06;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                              PRCT_LIMPO
PRCT_PERAM
RB21_LITRU
SUGA_ACHDO
RB31_LITRU
EOSI_HUMAN
FYRI_AMTEL
YLMI_YEAST
SIG4_LITRU
PSK_DAUCA
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15.518 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1612378 seqs, 512079187 residues
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Listing first 45 summaries
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Indels Length 4;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  Swartzman B., Kapoor S., Graham A.F., Meighen E.A.;

Swartzman B., Kapoor S., Graham A.F., Meighen E.A.;

"A new Vibrio fischeri lux gene precedes a bidirectional termination site for the lux operon.";

J. Bacteriol. 172:6797-6802 (1990).

-I. FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as substrate in the luciferase-catalyzed reaction.

-I. CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.

-I. PATHWAY: Bioluminescent fatty acid reduction system; second step.

-I. SIMILARITY: Belongs to the luxE family.
                 01-WAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
TISSUE=Egg;
MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
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Sepia officinalis (Common cuttlefish).
Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
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MEDLINE=20403899; PubMed=1094467; DOI=10.1006/bbrc.2000.3286;
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                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 3 AA; 374 MW; 6AA33030000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 275:217-222(2000).
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=9107226; PubMed=2254256;
(Rel. 21, Created)
(Rel. 21, Last seq
                                                                                    protein synthetase) (Fragment)
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Best Local Similarity
                                                                                                                              Vibrio fischeri.
                                                                                                                                                                                        NCBI_TaxID=668;
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1 IK 2
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P83568;
                                                                                                          Name=1uxE
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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                                                                                                                                                                                                              C.J.P.;
                                                                                                                                                                                    MEDLINE=93391436; PubMed=8397415;
McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Kamaide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
                                       MEDLINE=92028852; PubMed=1681803;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.,
Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
novel neuropeptide from sea anomones ";
Biochem. Biophys. Res. Commun. 179:1205-1211 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Gunn;
MEDINNE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
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Amidation; Direct protein sequencing; Neuropeptide.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
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$38636; AAB19259.1; -.
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                                                                                                                                                                                                                                                                                                                                   behaviour in sea anemones.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: Neuron specific.
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Local 2; Conserve
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Best Local Similarity
Matches 2; Conserv
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Browne N., Dowds B.C.A.; Submitted (JUL-2001) to Swiss-Prot. 5
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Aust. J. Chem. 49:555-953 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                            LICOLA LUDELIA (DEBETC TIPE ITOG).
Eukaryota, Hetazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-I- MASS SPECIFOMETRY: M#-599, METHOD=FASH; RANGE=I-5; NOTE=Ref.1.
Amphibian defense peptide; Direct protein sequencing.
SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
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       Zatylny C., Marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk sperm-
attracting peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
                                                                                                                                                                      0; Indels
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Last annotation update)
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Rubellidin 1.1.
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tes 1; Conserv
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-1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles. PIR; A32480; A33480.

D-amino acid, Direct protein sequencing; Hormone.

NOD RES.

2 D-phenylalanine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                             29.2%; Score 7; DB 2; Length 5; 50.0%; Pred. No. 1.6e+06; Live 1; Mismatches 0; Indelt
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5 AA; 623 MW; 6B01AAA336F00000 CRC64;
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4 AA; 408 MW; 6AADD9C81000000 CRC64;
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Biochem. Biophys. Res. Commun. 177:847-853(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Achatina fulica (Giant African snail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Ferussac; TISSUE-Heart atrium;
MEDLINE-91264856; PubMed-1675568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ferussac; TISSUE=Ganglion;
MEDLINE=89273551; PubMed=2597281;
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Conservative 0
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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4 AA.

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group.";
Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-- SUBCELLULAR LOCATION: Secreted.
-- TISSUE SPECIFICITY: Neuron specific.
-- TISSUE SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
PTR; A35779; A35779.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES.
                                                                                                                                                                                                                                                                                           SEQUENCE, AND MASS SPECTROMETRY.
MEDLINE=90319122; PubMed=1973541;
Grimmelikhuijzen C.J.P., Rinchart K.L. Jr., Jacob E., Graff D.,
Reinscheid R.K., Nothacker H.-P., Staley A.L.;
"Isolation of L.3-phenyllactyl-Leu-Arg-Aan-NH2 (Antho-RNamide), a sanemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                 Eukaryota, Metazoa; Cnidaria, Anthozoa; Zoantharia, Actiniaria, Nynantheae, Actiniidae, Anthopleura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 4 Asparagine amide.
4 AA; 549 MW; 64540729A0000000 CRC64;
                                                                                                                                                        (Rel. 41, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                                                                                          Anthopleura elegantissima (Sea anemone)
                                                                                                                                      (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
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                                                                                                      STANDARD;
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Matches 1: Conser
                                                                                                                                                      (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=89766;
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                                                                                                                                      28-FEB-2003
                                                                                                                                                                          05-JUL-2004
                                                                                                                                                        28-FEB-2003
                                                                                                      FLRN ANTEL P58707:
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SEQUENCE
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                                                                                    FLRN ANTEL
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MEDINE-9436417; PubMed=791248; DDI=10.1016/0196-9781(94)90166-X;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRPamide_related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N; BVARB B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; "Identification of RFamide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
                                                                                                                                                                                                                        MEDLINE=9219594; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
                                                                                                                                                                                                                                       Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.,
"Identification of RRamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
                                                                              FMRFamide-like neuropeptide YLRF-amide.
FMRFamide-like neuropeptide YLRF-amide.
Hivudo medicinalise (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hellsoma trivolvis (Snail).
Bukaryota; Meteazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBI_TaxID=6421, 27815;
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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4;
                                                                                                                                                                                                                                                                                                                                           Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
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MOD RES 4 4 Phenylalanine amide.

SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 1; Le
Pred. No. 1.6e+06;
                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                 4 AA.
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                 PRT;
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                 STANDARD;
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Best Local Similarity
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P42561;
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FLRF_HIRME
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--- SUBCELLIULAR LOCATION: Secreted.
--- PTTM: Ocp-2 has L-Phe instead of D-Phe.
--- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-amino acid; Direct protein sequencing; Hormone.

MOD RES 2 D-phenylalanine (in form Ocp-1) SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
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25.0%; Score 6; DB 1; Length 4; 50.0%; Pred. No. 1.6e+06; Live 1; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Cardioactive peptides Ocp-1/Ocp-2.
                                                                                                                                                                                                                                                                                                                                                                                                       4 AA
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SEQUENCE
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-!-SUBCELDULAR LOCATION: Secreted.
-!-PTM: Ocp-4 has D-Ser instead of L-Ser.
-!-MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
D-amino acid; Direct protein sequencing; Hormone.
MOD RES
2 D-serine (in form Ocp-4).
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Octopodiformes, Octopoda, Incirrata, Octopodidae, Octopus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO:0004872; F:receptor activity; IEA.
GO:0007264; P:small GTPase mediated signal transduction; IEA.
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                                                                                      Indels
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                            Length 4;
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4 AA; 463 MW; 6AB365B81000000 CRC64;
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EMBL: S64248; AAB20279.1; -.
HSSP; P01112; 1PLL.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                         DB 1; Len
5. 1.6e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
26-ULJ-2004 (Rel. 44, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
25.0%; Scc...
100.0%; Pred. No. ...
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nes 1; Conservative
                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Octopus minor (Octopus)
               Query Match
Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=89766;
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AC 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
DT 05-JUL-2004
DE Cardioactive
OS Octopus mino
OC Cutopus mino
OC Cutopus mino
OX NCBI_TAXID=8
RN [1]
RP SEQUENCE, SY
RC TISSUE=Brain
RX MEDLINE=2033
RA IWAKSHIE.,
RT Cardioactiv
RT Cardioactiv
RT Octopus mino
RL PEPTISE CC -1- FUNTION
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016047
01604 AC 01604 DT 01-NO 
                                                                                                                                                                                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJINE 99006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6; Shiuan D., Campbell A.; Transcriptional regulation and gene arrangement of Escherichia collistrobacter freundii and Salmonella typhimurium biotin oper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBL_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
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PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.
Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                       / Match 25.0%; Score 6; DB 2; Length 4; Local Similarity 100.0%; Pred. No. 1.6e+06; nes 1; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 6; DB 1; Length 5; 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0; Indelt
                                                                                         4 4 AA; 525 MW; 69CAB769A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase.
NON TER 5 5
SEQUENCE 5 AA; 582 MW; 6AAABIBIA6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 A.
InterPro; IPR001806; Ras_trnsfrmng.
PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: Pyridoxal phosphate.
-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
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Job time : 168 secs

us-10-047-945-3.closed.rag

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 19:41:29; Search time 157 Seconds (without alignments) 12.317 Million cell updates/sec

US-10-047-945-3 24 Title: Perfect score:

1 LKAMD 5 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

45841 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 5 8 8 8 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

first 45 summaries

genese@2000s:* genese@2001s:* genese@2002s:* genese@2003as:* genese@2003bs:* A Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		40				
Result No.	Score	Query Match	Length	DB	ID	Description
н	24	100.0	ស	7	AAW53842	Aaw53842 N-terminu
7	24	100.0	2	7	ABB80224	Abb80224 Synthetic
m	21	87.5	Ŋ	N	AAW24922	Aaw24922 Vesicular
4	16	66.7	4	7	ABR82923	Abr82923 Tetrapept
S	16	66.7	C)	ហ	AAM49579	Aam49579 Human bet
9	15	62.5	S	ო	AAY83346	Aay83346 Peptide m
7	15	62.5	5	4	AAM51285	
80	15	62.5	D	4	AAB35188	Aab35188 Human Tra
o	15	62.5	S	7	ADJ82602	Adj82602 Shuffled
10	15	62.5	ß	7	ADJ82644	Adj82644 Shuffled
11	15	62.5	_C	æ	ADM46700	Adm46700 C-termina
12	15	62.5	S	æ	ADM46839	Adm46839 Variant a
13	15	62.5	ß	œ	ADM46841	Adm46841 Variant a
14	15	62.5	S	æ	ADQ95007	Adq95007 Synthetic
15	14	58.3	4	~	AAR83230	Aar83230 Integrin-
16	14	58.3	4	~	AAY08030	Aay08030 Biotin de
17	14	58.3	4	m	AAY88365	Aay88365 CCR inhib
18	14	58.3	4	Ŋ	AAU74705	Aau74705 Human cel
19	14	58.3	S	7	AAR91816	Aar91816 Mab-425-C
20	14	58.3	S	4	AAM51340	Aam51340 Anti-HIV
21	14	58.3	S	Ŋ	ABB46284	Abb46284 Desmoglei
22	14	58.3	ιn	Ŋ	AA015010	Aao15010 Mutant VH
23	14	58.3	'n	7	ADF53341	-
24	13	54.2	4	~	AAW08855	Aaw08855 Peptide c
25	13	54.2	4	N	AAW48196	Aaw48196 Conantoki

Caspa Caspa Caspa Human Amino Pepti Pepti Antif Antif Antif Antif Antif Antif Apopt Amino Pepti Lys-h	Abg75419 BIVM N-te
2 AAW49978 2 AAY24412 3 AAY24412 4 AAY24511 4 AAG79033 4 AAB30767 4 AAB30767 4 AAB30767 5 ABB2672 6 ABB2672 6 ABG6448 8 ADD44013 8 ADD44013 8 ADD45983 2 AAW2550 3 AAW2550 7 AD110462	7 ABG75419
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ALIGNMENTS

LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment. AAW53842 standard; peptide; 5 AA. N-terminus of opossum LTNF. (first entry) 08-JUL-1998 AAW53842; AAW53842

Didelphis virginiana USS744449-A.

96US-00657163. 03-JUN-1996; 28-APR-1998.

93US-00058387. 94US-00310340. 10-MAY-1993; 22-SEP-1994;

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps FW, Lipps BV;

WPI; 1998-271108/24.

Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.

Claim 5; Col 13; 11pp; English.

Toxin Neutralising Factor (LTFF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the This sequence represents the peptide of the invention. It is a Lethal

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WPI; 1997-319066/29.
                                                                   Local Similarity
hes 5; Conserv
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                  Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-1990;
31-JAN-1991;
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17-OCT-1997
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                                                 Ouery Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosines (ADA). In particular, the methods of the invention are useful for diagnosing and trienting conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, dations or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins and election is relatively non-invasive when compared to blood collection for serum. Saliva proteins contrifung time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; ElE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
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                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                               .
                                                                                                           Length 5;
                                                                                                                                             Indels
                                                                                                         100.0%; Score 24; DB 2; I
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 3; 24pp; English.
                                                                                                                                                                                                                                                                                                            ABB80224 standard; peptide; 5 AA
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic LTNF, LT-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipps BV, Lipps FW;
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                                                                                                                                                                                 1 LKAMD 5 ·
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                                     to horse proteins
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                                                                                                                                                                                                                   LKAMD
                                                                       Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Etiological agent; autoimmune disease; systemic lupus erythematosus; SLE; Ro/SSA; immunoreactive; autoantibody; antigenicity; nucleocapsid;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vesicular stomatitis virus nucleocapsid protein #2.
100.0%; Score 24; DB 7; 100.0%; Pred. No. 1.8e+06;
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                             AAW24922 standard; peptide; 5 AA.
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(first entry)
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                                                                       Conservative
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The invention relates to increasing or reducing cell apoptosis. The method involves providing at least 1 cell or a tissue, and a polypeptide method involves providing at least 1 cell or a tissue, and a polypeptide content of many and administering the polypeptide to the cell so that apoptosis of the cell or tissues is increased or reduced. The polypeptide is selected from ABR8223-28 and administering the polypeptide to the cell so that apoptosis of the cell or tissues is increased or reduced. The polypeptide is selected from cell or tissues is nethods and compositions are useful for diagnosing, (CEBPbeta). The methods and compositions are useful for diagnosing. The fibrosis is hepatic, lung, kidney or ocular fibrosis, where the hepatic fibrosis is the associated with rejection of liver transplant, hepatitis C infection, chart that a wound, burn, trauma, environmental toxin or ischaemia, or with a disease in a lung, kidney or ocular tissue. The cell apoptosis conditions also associated with a liver disease from rejection of liver transplant, hepatitis C infection, hepatitis B infection, alcoholism, toxic liver disease, penetic chaemochromatosis and porphyria. The fibrosis or cell apoptosis is also associated with brain gliosis, Alzheimer's disease, hepatic disease, brain damage, neurological trauma, the fibrosis conditions and fibrotic pulmonary disease. The present sequence represents a tetrapeptide obtained from exemplary mouse and human controlled to the exemplary controlled to the exemplace of the exemp
                                                                                                                                                                                                                                                     C/BBPbeta; apoptosis; CCAAT/enhancer binding protein; hepatotropic; virucide; vulnerary; vasotropic; nephrotropic; ophthalmological; cytostatic; cerebroprotective; neuroprotective; antiarteriosclerotic; cardiant; nootropic; human; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing or reducing cell apoptosis, for diagnosing, preventing and treating cancer, fibrosis, ischemia, Alzheimer's disease, myocardial infarction and arteriosclerosis, comprising using novel tetrapeptide
                                                                                                                                                                                                       Tetrapeptide sequence derived from C/EBPbeta polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 66.7%; Score 16; DB 7; Length 4; Local Similarity 75.0%; Pred. No. 1.8e+06; neg 3; Conservative 1; Mismatches 0; Indels
                                                ABR82923 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 79; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2003; 2003WO-US005141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002; 2002US-0358764P.
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buck M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-721701/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003072031-A2.
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chojkier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2003
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                                                                                                   ABR82923;
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RESULT 4
                          ABR82923
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and/or

New defensin type peptides useful for treatment of bacterial infections and for fertility control, and as a diagnostic marker of inflammatory disease in epithelial organs.

Claim 4; Page 22; 41pp; German.

Adermann K;

Conejo-Garcia J,

Forssmann W,

WPI; 2002-179697/23.

(IPFP-) IPF PHARM GMBH

11-JUL-2001; 2001WO-EP007973. 11-JUL-2000; 2000DE-01033505.

WO200204487-A2.

17-JAN-2002

Homo sapiens.

Defensin; human; antibacterial; antiinfertility; contraceptive; peptide therapy; infection; gastrointestinal; respiratory tract; urogenital tract; skin; gland; sperm penetration; systemic disease; infertility; sperm inidation; sperm maturation; diagnostic marker; inflammatory disease; epithelial organ; gene therapy.

Human beta-defensin hBD-7 peptide fragment #2.

(first entry)

28-MAY-2002

AAM49579;

AAM49579 standard; peptide; 5 AA.

RESULT 5 AAM49579

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This invention describes novel peptides (1) of the defensin type which have antibacterial, antiinfertility and contraceptive activity and which can be used for peptide therapy. (1), and their derivatives and can be used for peptide therapy. (1) and their derivatives and cassociated will be treat bacterial infections, particularly of the gastrointestinal, respiratory or urogenital tracts, or of the skin coverexpression or deficiency of defensin production, particularly as ubstitution therapy or by using (1)-specific antibodies; (ii) to treat infertility, sepecially where the result of disordered sperm penetration, infation or maturation, also as contraceptives, and (iv) as a diagnostic marker of inflammatory disease in epithelial organs. Both chronic and coute diseases may be treated, e.g. in intensive care. Also genes that canced (1) can be used for systemic or localised gene therapy of the specified diseases, in epithelial tissues or organs. (1) have exceptional consistence are particularly well suited for long-term use. This sequence response, they are particularly well suited for long-term use. This sequence represents
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1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 16; DB 5; Length 5; 60.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY83346 standard; peptide; 5 AA.
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Best Local Similarity
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ID AAY8
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Gaps ö

KAMD 5

Best Loc Matches

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AAY83346;

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The invention relates to peptides (AAMS1251-AAMS1381) with a higher affinity to gp120, part of the outer shell of HIV, than known peptides. CC affinity to gp120, shown by formula (H-)-Ha-A3-A4-A5-R. C(1), A1-A2-A3-A4-A5-R. (2) or H-A1-A2-A3-A4-A5-R. (3), (H-)-a1-a2-a3-a4-A5-R. (2), A1-A2-A3-A4-A5-R. (3), CH-) a1-a2-a3-a4-A5-R. (2), A1-A2-A3-A4-A5-R. (3), CH-) a1-a2-a3-a4-A5-R. (5) or H-A1-A2-A3-A4-A5-R. (6). A1 = ASp. CC Lys. Val. Glu, Gly, Asn or Tyr residue, A2 = A3-A3-A5-R. (6). A1 = ASp. CC Lie, Leu or Tyr residue; A3 = Lys. Asy, Arg, And or Tyr residue; A3 = Lys. Arg, Phe. Trp. Pro or Tyr residue, R = OH derived CC Asp. Glu, His. Lys. Arg, Phe. Trp. Pro or Tyr residue R = OH derived C Tyr Val. Glu, Gly, Asn or Tyr residue, or a polypeptide residue having optional amino acids at N-terminal, A5. = Gly, A1. Leu, I1e, Ser, CThr. Met, Asn. Gln, His. Lys. Arg, Phe. Trp, Pro or Tyr residue, or a polypeptide residue having optional amino acids at C-terminal; a1 = Tyr. C Thr. Met, Asn. Gln, His. Optional amino acids at C-terminal; a1 = Tyr. C Thr. His or Lys residue; a3 = Lys. Tyr. Arg, Gln, His, Lys. Arg, Phe or Tyr Arg, Trp, His or C Try residue; a5 = Gly, A1, Leu, I1e, Ser, Thr. Met, A3, A1, Val, Leu, His. C Tyr residue; a1 = Tyr. Arg, Phe, Tyr or Try residue; a1 = Tyr. Arg, Phe, Tyr or Try residue; a1 = Tyr. Arg, Phe, Tyr or Try residue; a1 = Tyr. Arg, Phe, Tyr or Try residue having optional amino acids at C terminal; and a5' = Gly, A1a, Val, Leu, I1e, Ser, Thr. Met, Asn. Gln, His or Asp residue, or a polypeptide residue having optional amino acids at C-terminal; and a5' = Gly, A1a, Val, Leu, I1e, Ser, Thr. Met, Asn. Gln, His or His, Lys, Arg, Phe, Tyr or Try or Try, or a Dolypeptide residue having optional amino acids at C-terminal; and a5' = Gly, A1a, Val, Leu, I1e, Ser, Thr. Met, Asn. Gln, A1a, Val, Leu, I1e, Ser, Thr. Met, Asn. Gln, A1a, Val, Leu, I1e, Ser, Thr. Met, Asn. Gln, A1a, Val, Leu, I1e, Ser, Thr. Met, Asn. Gln, His, Lys, Arg, Phe, Tyr or Try, or Try 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; protein degradation; siah-mediated degradation protein; SMDP; SCF-complex protein; SCP; siah-latlpha; siah-latine protein; SCP; SkP;-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division; Skpl-associated destruction-box protein; inflammatory disease.
                                                                                                                                                                                                               Novel peptides with affinity to gp 120, useful for treatment of HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15; DB 4; Length 5;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Traf 6 aptamer clone peptide SEQ ID NO: 39.
                                                                                                                                                                                                                                                                       Example 2; Page 8; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB35188 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%;
11-JAN-2000; 2000JP-0006182.
                                                    11-JAN-2000; 2000JP-0006182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Conservative
                                                                                                                                                           WPI; 2001-605354/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5 AA;
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                                                                                                            (FUJI/) FUJII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences encoding SDD1, a subtilisin-like serine protease, can be used to produce transgenic plants with altered stomata characterisitics. These plants exhibit improved freshness, increased dry weight, reduced leaf temperatures, reduced water loss and lower water consumption and for enhancing the sugar and/or protein content of plant leaves, modulating photosynthesis under high intensity conditions or for the improvement of disease resistance of plants. The transgenic plants and cells of such plants are useful in the preparation of feed, food or additives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant DNA molecules encoding subtilisin-like serine protease, useful for producing transgenic plants with altered stomata, lower water consumption and enhanced diseased resistance.
                                                                                                                                                           SDD1; serine protease; subtilisin; transgenic plants; dry weight; stomata; sugar; water; protein; CO_2; H_2O; CO2; H2O; crop protection; feed; foodstuffs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                      Peptide motif of SDD1 subtilisin-like serine protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-EP007633
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                                                    (first entry)
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                                                                                                                                                                                                                                                                    Synthetic.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berger D, Altmann T;
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Best Local Similarity
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                                                    16-AUG-2000
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Gaps

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09-JUN-2000; 2000WO-US015873.

JP2001192399-A.

AAM51285;

RESULT 7

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17-JUL-2001

99US-00330517

11-JUN-1999;

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RESULT 10
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                                                                                                           The present invention provides the protein and coding sequences of several siah-mediated degradation proteins and SCF-complex proteins. These are designated Siah-lalpha, Siah-l interacting protein (SIP), which encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skplassociated F-box protein-lalpha and beta and -2 (SAF-lalpha, SAF-lbeta and SAF-2) and Skplassociated destruction-box protein (SAD). The proteins and their coding sequences are useful in the diagnosis and treatment of cancers, disorders where too little cell division occurs such as bone marrow aplasias, immunodeficiencies and inflammatory diseases including sepsis, fibrosis, arthritis and graft versus host
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
                                                           Siah-Mediated Degradation Protein, useful for drug screening, for therapeutic applications and for functional genomics.
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                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                 Length 5;
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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                                                                                          Example 15; Page 71; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuffled KLMSY peptide #13.
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
3, Conservative
                    Matsuzawa S;
(BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dean C, Heidaran M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HAAL/) HAALAND P D.
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                                       WPI; 2001-071273/08
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                                                                                                                                                                                                                                           Sequence 5 AA;
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                   Reed JC,
                                                                                                                                                                                                                        disease
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New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; asrcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastcoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
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                                                                                                                                                                                                                                                                                                                                                         . 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 7
Pred. No. 1.8e-1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 425; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ82644 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BECT ) BECTON DICKINSON & CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-2002; 2002WO-US031165.
                                                                                                                                                                                                                                                                                                                                                   62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shuffled KLMSY peptide #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HAAL/) HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-505179/47
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                                                                                                                                                                                                                                                                                                             Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAM
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Variant antibody variable domain peptide, C-terminal of CDRH3
                                                               ADM46839 standard; peptide; 5 AA.
                                                                                                                03-JUN-2004 (first entry)
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     AMD
                                                                                                                                                                                                   Unidentified
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Lys-Lys (P4) Phe-Phe-His-Pro-val (P5) . (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glloma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (anglogenic) disorders. This sequence represents a shuffled P3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide useful for selecting antigen for antigen binding variable domain that binds to target antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel polypeptide comprising a variant CDRH3 antibody variable domain. The invention further provides an antibody phage library. The variant CDRH3 polypeptide is useful for selecting an antigen for an antigen binding variable domain that binds to a target. The phage library is useful for selecting a polypeptide that binds to a target attigen from the library of polypeptides and isolating high affinity binders to a target antigen from the library of polypeptides and isolating high expression vectors. This sequence represents a variable antibody domain related polypeptide of the invention.
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                                                                                                                                                                Gaps
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                                                                                                                           Score 15; DB 7; Length 5;
Pred. No. 1.88+06;
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llarity 100.0%; Pred. No. 1.6
Conservative 0; Mismatches
                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                          ADM46700 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                      domain; phage; library; antigen
                                                                                                                                       62.5%;
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16-APR-2003; 2003US-0463656P.
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                 C-terminal CDRH3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                     1 LKSM 4
                                                                                                                                                                                       1 LKAM 4
                                                                                                                                                                                                                                                                                                                                                                         variant; CDRH3;
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                                                                                                                Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
variant; CDRH3; CDR; complementarity determining region; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variant; CDRH3; CDR; complementarity determining region; antibody;
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 163; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain that binds to target antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46841 standard; peptide; 5 AA.
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                             domain; phage; library; antigen
                                                                                                                                                                                                                                                     03-JUN-2003; 2003WO-US017545.
                                                                                                                                                                                                                                                                                                             03-JUN-2002; 2002US-0385338P
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                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sidhu SS;
                                                                                                                                         WO2003102157-A2.
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This invention relates to a novel polypeptide comprising a variant composition and all deat one structural amino acid position, and at least one structural amino acid position, and at least one non-structural position having a variant amino acid. The invention is non-structural position having a variant amino acid. The invention is useful for designing a CDRH3 scaffold and the polypeptides are useful as a source for identifying novel antigen binding polypeptides are useful as a source for identifying novel antigen binding polypeptides and antibody variable domains that can be used therapeutically or as reagents. A synthetic antibody phage library of these polypeptides is useful for screening synthetic antibody or antigen binding polypeptide with a strength as resource for identifying immunoglobulin polypeptide sequences that are capable of interacting with any of a wide variety of target molecules. The invention provides high throughput, variety of target molecules. The invention provides high throughput, of interest. The present sequence is that of a peptide which is related to the novel polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cysteine contg. peptide derivs. Which inhibit platelet integrin - are useful for treating or preventing circulatory disease, thrombosis, etc., also for affinity purification. of integrins.
                                New polypeptide comprising variant complementarity determining region of heavy chain 3 having structural amino acid positions, and non-structural positions having variant amino acid, useful for identifying antigen binding polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelet integrin; gp IIb/IIIa; thrombosis; infarction; inflammation; coronary heart disease; arteriosclerosis; atherosclerosis; stroke; angina pectoris; tumour; osteoporosis; anglogenesis; restenosis; awound healing; ligand; integrin; affinity chromatography.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 15; DB 8; Length 5; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indels
                                                                                                                Disclosure; SEQ ID NO 4; 238pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin-inhibiting peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felding-Habermann B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93DE-04336758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-171142/23.
 WPI; 2004-580713/56.
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les 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5 AA;
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Matches
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                                                                                                                                                                                                                                                                New polypeptide useful for selecting antigen for antigen binding variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementarity determining region; heavy chain 3; CDRH3, CDRH3 scaffold; synthetic antibody phage library; binding affinity; structural stability;
                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel polypeptide comprising a variant CDRH3 antibody variable domain. The invention further provides an antibody phage library. The variant CDRH3 polypeptide is useful for selecting an antigen for an antigen binding variable domain that binds to a target. The phage library is useful for selecting a polypeptide that binds to a target antigen from the library of polypeptides and isolating high affinity binders to a target antigen from the library of polypeptides and isolating high expression vectors. This sequence represents a variable antibody domain related polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic phage antibody library-related 4D5 antibody peptide SeqID4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                              domain that binds to target antigen.
                                                                                                                                                                                                                                                                                                                Disclosure; Page 7; 205pp; English
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18-JUL-2003; 2003US-0488610P.
08-OCT-2003; 2003US-0510314P.
                                                                                                             03-JUN-2002; 2002US-0385338P.
16-APR-2003; 2003US-0463656P.
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                                                                                03-JUN-2003; 2003WO-US017545
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Best Local Similarity 100.
                                                                                                                                                               (GETH ) GENENTECH INC
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                                                                                                                                                                                               Sidhu SS;
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               WO2003102157-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Unidentified.
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                                               11-DEC-2003
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The invention relates to new linear peptides of formula X-A-Cys(R1)-B-Z in which X is H or Ac; A is absent or is Asp or a specified polypeptide; B is absent or a specified amino acid or polypeptide; A and B cannot both be absent; and Z is OH or an ester or amide group. The peptides inhibit binding of the platelet integrin gpIIb/IIIa to its natural ligands and so are useful for preventing circulatory diseases, thrombosis, cardiac infarction, inflammation, coronary heart disease, arteriosclerosis, attherosclerosis, stroke, angina pectoris, tumour, osteoporosis, anglogenesis and restenosis. They are also useful for promoting healing of wounds and as ligands for purification of integrins by affinity chromatography. The present sequence is a specific example of the X888888888888888888888888

Sequence 4 AA;

Gaps ö Query Match 58.3%; Score 14; DB 2; Length 4; Best Local Similarity 75.0%; Pred. No. 1.8e+06; Matches 3; Conservative 0; Mismatches 1; Indels

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Search completed: May 26, 2005, 19:56:21 Job time : 165 secs

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1: /cgm2_6/prodata/1/pubpaa/NSO7_PUBCOMB.pep:*
2: /cgm2_6/prodata/1/pubpaa/NSO6 NEW PUB.pep:*
4: /cgm2_6/prodata/1/pubpaa/NSO6 NEW PUB.pep:*
5: /cgm2_6/prodata/1/pubpaa/NSO6 NEW PUB.pep:*
5: /cgm2_6/prodata/1/pubpaa/NSO7_NEW PUB.pep:*
6: /cgm2_6/prodata/1/pubpaa/NSO7_NEW PUB.pep:*
7: /cgm2_6/prodata/1/pubpaa/NSO8_NEW PUB.pep:*
8: /cgm2_6/prodata/1/pubpaa/NSO8_NEW PUB.pep:*
9: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
9: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
10: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
11: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
12: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
13: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
14: /cgm2_6/prodata/1/pubpaa/NSO8_PUBCOMB.pep:*
15: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
16: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
17: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
18: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
18: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgm2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1462099 segs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                         US-10-047-945-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKAMD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	3, Appli	39, Appl	107, App	4, Appli	7, Appl	7, Appl	17, Appl	6, Appl	2, Appli	2, Appli	9, Appli	33, Appl	88. Appl
Description	Sequence	Sequence	Sequence 107, App	Sequence	Sequence 1	Sequence 1	Sequence	Sequence 2	Sequence	Sequence	Sequence	Sequence 33, Appl	Segmence
Ω	US-10-047-945-3	US-10-679-246-39	US-10-783-311-107	US-10-759-731A-4	US-09-016-750C-17	US-09-016-869B-17	US-09-947-206-17	US-09-817-661-26	US-10-099-442-2	US-10-911-065-2	US-10-115-704-9	US-10-357-467-33	US-10-808-187-88
DB	14	16	17	11	6	6	10	6	14	17	13	14	17
% Query Match Length DB	5	ß	S	Ŋ	4	4	4	Ŋ	S	2	4	4	4
% Query Match	100.0	62.5	62.5	62.5	58.3	58.3	58.3	58.3	58.3	58.3	54.2	54.2	54.2
Score	24	15	15	15	14	14	14	14	14	14	13	13	13
Result No.	1	7	m	4	S	9	7	8	6	10	11	12	13

ce 93 ce 59 e 110 e 5,	2004 1811 2004 1811	Sequence 75, Appl Sequence 75, Appl Sequence 437, Appl Sequence 437, Appl Sequence 437, Appl Sequence 22, Appl Sequence 12, Appl Sequence 22, Appl Sequence 22, Appl Sequence 251, Appl
-156-21 -417-47 782-980 915-306 915-306	9 US-09-915-374- 9 US-09-915-374- 9 US-09-915-374- 9 US-09-915-374- 14 US-10-214-932 15 US-10-435-751 16 US-10-435-751 16 US-10-806-018 8 US-08-425508 9 US-09-915-376- 10 US-09-915-376-	US-09-788 US-10-006 US-10-006 US-10-395 US-10-395 US-10-346 US-10-346 US-10-348 US-10-348 US-10-348 US-10-712 US-10-938
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ALIGNMENTS

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ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
                                                                                             APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (195) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE:
FRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 3
LENGTH: 5
LENGTH: 5
TYPE: PRICE
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 24; DB 14; Length 5; Best Local Similarity 100.0%; Pred. No. 1.3e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                    Sequence 3, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: SYNTHESIZED. ) OTHER INFORMATION: US 5,576,297. US-10-047-945-3
JS-10-047-945-3
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NAME/KEY:
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Gaps ö

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SERUM

1 LKAMD 5 1 LKAMD ઠે 셤

Indels

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GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serranc, Manuel
APPLICANT: Serranc, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,750C
FILING DATE: 30-JAN-1998
RIGH APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-JUL-1997
PRIOR APPLICATION NUMBER: US 08/306,511
PRIOR APPLICATION NUMBER: US 08/306,511
PRIOR APPLICATION NUMBER: US 08/248,812
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
PRIOR APPLICATION NUMBER: US 08/227,371
                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 15; DB 17; I
100.0%; Pred. No. 1.3e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: C-terminal of CDRH3 of 4D5 US-10-759-731A-4
PRIOR APPLICATION NUMBER: US 60/441,059
PRIOR FILING DATE: 2003-01-16
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 194
SOFWARE: Patentin version 3.3
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: FOLEY, HOAG & ELIOT LLP
One Post Office Square
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APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
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APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
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FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09016750C Patent No. US20020025305A1
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 3; Conservative
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STREET: CAL.
THY: BOSTON
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                                                                                                                                                                                                                       LENGTH:
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                                             Sequence 39, Application US/10679246
Publication No. US20040163138A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Read, John C.
APPLICANT: Matsuzawa, Shu-ichi
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: 66821-235
CURRENT APPLICATION NUMBER: US/10/679,246
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2000-06-09
PRIOR PLING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Bond, Christoper J.
TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES
FILE REFERENCE: 11669.136USU1
CURRENT APPLICATION NUMBER: US/10/759,731A
CURRENT FILING DATE: 2004-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 62.5%; Score 15; DB 16; L Similarity 100.0%; Pred. No. 1.3e+06; 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetically generated peptide US-10-783-311-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; L 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQUENCE 107, Application US/10783311
FUBLICATION NO. US20050009136A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: PAPP-A LIGANDS
TILLE REFERENCE: 10280-059001
CURRENT APPLICATION NUMBER: US/10/783,311
CURRENT FILING DATE: 2004-02-19
PRIOR FILING DATE: 2004-02-19
PRIOR FILING DATE: 2003-0-19
NUMBER OF SEQ ID NOS: 394
SOFTWARE: FREEEEQ for Windows Version 4.0
SEQ ID NO 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.5%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 3; Conservative 0; Mismatches
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Publication No. US20050079574A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo Bapien
US-10-679-246-39
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Best Local Similarity
Matches 3; Conserv
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US-10-759-731A-4
                           US-10-679-246-39
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2 KAMD 5
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APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Serrano, Manuel.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Ropes & Gray
STREET: One International Place
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.3%; Score 14; DB 9; Best Local Similarity 75.0%; Pred. No. 1.3e+06; Matches 3; Conservative 0; Mismatches 1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09945
FILING DATE: 18 -0CT-1993
ATTORNY AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.13
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
INFORMATION FOR SEQ 1D NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acid
STRANDENNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTIE USAS

ZIF: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/893, 274
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893, 274
FILING DATE: 15-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248, 812
FILING DATE: 14-SEP-1994
FILING DATE: 12-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248, 812
FILING DATE: 14-SEP-1994
FILING DATE: 18-NOV-1993
FILING DATE: 18-NOV-1993
FILING DATE: 18-NOV-1993
FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09016869B Patent No. US20020082392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-09-016-750C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MA
USA
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Gaps
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US-09-17
US-09-17, Application US/09947206
Sequence 17, Application US/09947206
Publication No US20030100489A1
GENERAL INFORMATION:
Demetrick, David H.
Serrano, Manuel
Hannon, Manuel
Standon Gregory J.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,206
FILING DATE: 04-Sep-2001
PRIOR APPLICATION NUMBER: 09/016,750
FILING DATE: 1998-01-03
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
APPLICATION NUMBER: US 08/227,371
FILING DATE: 34-APR-1994
APPLICATION NUMBER: US 08/227,371
FILING DATE: 4-APR-1994
APPLICATION NUMBER: US 08/227,371
                                                                                                                                                                                                                                                                                                                                                                                     58.3%; Score 14; DB 9; L
75.0%; Pred. No. 1.3e+06;
tive 0; Mismatches 1;
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: G6,719
TELECOMMUNICATION INFORMATION:
TELEFRANE: (617) 951-739
TELEFRANE: (617) 951-7050
INFORMATION FOR SEQ ID No: 17:
SEQUENCE CHARACTERISTICS:
LENOTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-OCT-1992
APPLICATION NUMBER: PCT/US93/09945
FILING DATE: 18-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 07/991,997
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APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.v.
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-016-869B-17
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Gaps
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                                                                                                                    58.3%; Score 14; DB 14; Length 5; 100.0%; Pred. No. 1.3e+06; ive 0; Mismatches 0; Indels
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Publication No. US20020192780A1

GENERAL INFORMATION:
APPLICANT: SCHN, JOON HONG
TITLE OF INVENTION: NOVEL ANTI-INFLAMMATORY, PEPTIDES
FILE REPREBNCE:
CURRENT APPLICATION NUMBER: US/10/115,704

CURRENT FILING DATE: 2002-06-05

PRIOR PILING DATE: 2001-04-21

NUMBER: OF SEQ ID NOS: 11

SOFTWARE: Kopatent in 1.71

SOFTWARE: Kopatent in 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%; Score 14; DB 17;
100.0%; Pred. No. 1.3e+06
tive 0; Mismatches 0
                                                                   ) OTHER INFORMATION: Synthetic sequence. US-10-099-442-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INPORMATION: SYNTHETIC
                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                             3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
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LENGTH: 5
                                                      FEATURE:
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Sequence 2, Application US/10099442
Sequence 2, Application US/10099442
Sequence 2, Application US. US20030129604A1
GENERAL INFORMATION:
APPLICANT: Worg, GOTGON G.
APPLICANT: Langer-Safer, Pennina
TITLE OF INVENTION: Identification of Molecular Sequence Signatures and Methods Invol
TITLE OF INVENTION: Same
FILE REFERENCE: 3016.2A
CURRENT APPLICATION NUMBER: US/10/099,442
CURRENT FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-05-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                    Length 4;
                                                                                                                                                                                                                                  58.3%; Score 14; DB 10; Length 4; 75.0%; Pred. No. 1.3e+06; ive 0; Mismatches 1; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 14; DB 9; Length 5; 50.0%; Pred. No. 1.3e+06; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Osbourn, Jane
APPLICANT: Holet, Thor
TITLE OF INVENTION: Improvements to ribosome display
FILE REFERENCE: 84633
                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/817,661
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/193,802
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09817661
Patent No. US20020076692A1
GENERAL INFORMATION:
                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                               TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                        LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 2; Conservative
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Sequence 93, Application US/10156214A

Publication No. US2004001801A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edwin L. Madison
APPLICANT: George P. Vlasuk
APPLICANT: George P. Vlasuk
APPLICANT: Mallareddy Komandla
APPLICANT: Mallareddy Komandla
APPLICANT: Daniel Vanna Siev
ITILE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic Us
ITILE OF INVENTION: Thereof
ITILE OF INVENTION: Thereof
ITILE OF INVENTION: 1010166,214A
CURRENT APPLICATION NUMBER: US/10/156,214A
CURRENT PILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 611
SEQ ID NO 93
LENGTH: 5
LENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Human severe acute respiratory system virus US-10-808-187-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%; Score 13; DB 17; I 100.0%; Pred. No. 1.3e+06;
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Best Local Similarity
Matches 3; Conserva
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                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FIGURY GENERAL COMPUTER: FIGURY GENERAL SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APELICATION DATA: APPLICATION NUMBER: US/10/357,467 FILING DATE: 04-Feb-2003 PRIOR APPLICATION NUMBER: WS 09/142,080 FILING DATE: 15-MAY-2000 APPLICATION NUMBER: WD 0897/12618 FILING DATE: 11-JUL-1997 APPLICATION NUMBER: WS 08/684,742 APPLICATION NUMBER: US 08/684,742 APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Manbeck, p.c.
STREET: 1425 K Street, N.W., Suite 800
                                                            Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
                                                                                                                1; Indels
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                                                      54.2%; Score 13; DB 13;
50.0%; Pred. No. 1.3e+06;
ive 1; Mismatches 1.
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REPERENCE/DOCKET NUMBER: 2314-256.A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cruz, Lourdes J.
Olivera, Baldomero M.
Walker, Craig
Colledge, Clark
Hillyard, David R.
Jimenez, Elsie
TITLE OF INVENTION: Conantokins
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/10357467
Publication No. US2030194729A1
GENERAL INFORMATION:
APPLICANT: Abogadie, Fe C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 33
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                    Query Match
Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                 2 KAMD 5
| :|
1 KVLD 4
                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-357-467-33
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US-10-115-704-9
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Sequence 59, Application US/10417476

Publication No. US20040002102A1

GENERAL INFORMATION:

APPLICANT: Littuan, Gary W.

APPLICANT: Hawke, No. US20040002102A11 A.

APPLICANT: Asson, Donna D.

APPLICANT: Rason, Donna D.

TITLE OF INVENTION: Transcriptional Products, and Uses Thereof

FILE REFERENCE: US-103X

CURRENT FILING DATE: 2003-04-16

NUMBER OF SEQ ID NOS: 64

SEQ ID NO S9

LENGTH: 5

LENGTH: 5

LENGTH: 5

LENGTH: 5

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LENGTH: 5
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                                                                                                                                                                                                                                                                                           0; Gaps
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54.2%; Score 13; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%; Score 13; DB 15; Length 5; 50.0%; Pred. No. 1.3e+06; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: BIVM N-terminus region of homology
                                               FEATURE:

DOME/KEY: MOD_RES

LOCATION: 1

COTHER INFORMATION: Xaa is H-D-Val

FEATURE:

NAME/KEY: MOD_RES

LOCATION: 5

COTHER INFORMATION: Alanine-therapeutic agent
US-10-156-214A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: May 26, 2005, 20:12:33
Job time : 172 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)...(3)
COTHER INFORMATION: Xaa = Val or Cys
US-10-417-476-59
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                 FEATURE:
OTHER INFORMATION: Conjugate
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Best Local Similarity 50.0°
Matches 2; Conservative
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2 KXLD 5
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2 LKA 4
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US-10-417-476-59
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION 5.14
PRIOR APPLICATION DATA:
APPLICATION SI4
PRIOR APPLICATION 5.14
PRIOR APPLICATION 5.14
PRIOR APPLICATION SI4
APPLICATION INMBER: 08/310,340
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
TELERENOR/DOCKET WUMBER: FWL-PAT-US-011
TELEBEAK: 713-463-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDENESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 3
ANTI-SENSE: NO
FRAGMENT TYPE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Applisequence 413, Appl Sequence 413, Appl Sequence 4, Applisequence 88, Applisequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 2, Applisequence 2, Applisequence 1128, Appl Sequence 34, Appl Sequence 33, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             May 26, 2005, 19:50:26 ; Search time 40 Seconds (without alignments) 9.331 Million cell updates/sec
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Sequence 5
Sequence 4
Sequence 1
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Sequence
Sequence
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(cgn2_6/ptodata//iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RDECTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-355-198-20

US-08-350-260A-413

US-09-104-337A-413

US-08-129-820-4

US-08-329-820-4

US-08-329-820-8

US-08-31-918A-17

US-08-31-147B-17

US-08-31-147B-17

US-08-31-147B-17

US-08-31-1481-2

US-08-31-1481-2

US-08-31-1481-2

US-08-31-1481-2

US-08-31-1481-2

US-08-31-1481-2

US-08-142-078-31

US-08-142-078-31

US-08-142-078-31

US-08-142-078-31

US-08-141-31

US-08-142-08-31

US-08-147-7774-16

US-08-477-777A-41
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PCT-US93-12679-40
US-08-208-108-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                         US-10-047-945-3
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Match Length I
                                                                                                                                                                                                                                                                                                                                1 LKAMD 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 5
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                                                                                                                                                                  Run on:
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No.
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amino acid
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Sequence 20, Application US/08335198

Patenn No. 5637454

GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18 PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION NUMBER: US/08/335,198
FILING DATE:
CHASSIFICATION UNFORMATION:
TELECOMMUNICATION UNFORMATION:
THE TOWN TOWN OF THE TOWN 
                                                                                                Length 5;
                                                                                                                                                       0; Indels
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                                                                                          100.0%; Score 24; DB 1; I
100.0%; Pred. No. 4.1e+05;
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US-08-350-260A-413
; Sequence 413, Application US/08350260A
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         SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 87.5
Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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FRAGMENT TYPE: internal
ORIGINAL SOURCE:
; ORIGINAL SOURCE:
US-08-657-163A-3
                                                                                                                                                                                                                1 LKAMD 5
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APPLICANT WHITE, Gregory Paul
APPLICANT: Winter, Gregory Paul
APPLICANT: Winter, Gregory Paul
APPLICANT: Winter, Gregory Paul
APPLICANT: Winter, Gammal Cameron
APPLICANT: Winter, Manchaue Pereror
APPLICANT: Winter, Manchaue Pereror
APPLICANT: Winter, Manchaue Cameron
APPLICANT: Winter, Manchaue Winter, Manchaue Cameron
APPLICANT: Winter, Manchaue Winter, Manchaue Cameron
ADDRESSER: David W. Clough
ANTORNEY, CLOUGH
ADDRESSER: David W. Clough
ATTORNEY, CLOUGH
ADDRESSER: David W. Clough
ATTORNEY, CLOUGH
ATT
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APPLICANT: John C. Reed
APPLICANT: John C. Reed
APPLICANT: Shu-ichi Matsuzawa
TITLE OF INVENTION: Mucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: P-LJ 4220
CURRENT APPLICATION NUMBER: US/09/591,694
CURRENT APPLICATION NUMBER: US/09/390,517
EARLIER APPLICATION NUMBER: US/09/330,517
EARLIER PILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 39
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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US-09-591-694-39
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                   Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15; DB 4; Length 5; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 413:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 31-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 13-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 13-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 413: US-09-104-337A-413
                   Sequence 413, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Materhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KAMD 5
US-09-104-337A-413
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                                     Gaps
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                                                                                                                                       US-08-329-820-4

US-08-329-820-4

Sequence 4, Application US/08329820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: DONCZYK, ALFRED

APPLICANT: DIEFENBACH, BEATE

APPLICANT: BIPPWANN, FRIEDRICH

ITILE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-0CT-1994

CLASSIFICATION NUMBER: DE 4336758.5

FILING DATE: 28-0CT-193

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

REFERENCE/DOCKET NUMBER: 33,302

REFERENCE/DOCKET NUMBER: 33,302

TELEPHONE: 703-243-6433

INFORMATION FOR SEO ID NO.
                                   Indels
62.5%; Score 15; DB 4; Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, Indels
                   Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 1;
Pred. No. 4.1e+05;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%;
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Best Local Similarity 75.0
Matches 3; Conservative
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; Sequence 39, Application US/09591694

RESULT 5 US-09-591-694-39

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                                                                                                                                                                                                                                                                                                                                                                                            COUNTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: POPPY disk
COMPUTER: IBM PC COMPALIDE
SOSTWARE: WORDERA
SOSTWARE: WORDERA
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,147
FILING DATE: 25-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APPL-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-A-APPL-1994
PRIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-346-147B-17
Sequence 17, Application US/08346147B
Patent No. 6211334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KAMD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                          Sequence 88, Application US/08329820
; Sequence 88, Application US/08329820
; Patent No. 5747457
; GENERAL INFORMATION:
APPLICANT: FILDING-HABERMANN, BRUNHILDE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION NUMBER: DE 4336758.5
FILING DATE: 23-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: MERCK 1635
TELECOMMUNICATION NUMBER: MERCK 1635
TELECOMMUNICATION NUMBER: MERCK 1635
TELECOMMUNICATION NUMBER: MARCK 1635
TELERAC 703-243-6410
INFORMATION FOR SEQ ID NO: 68:
SEGUENCE CHARACTERICES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.3%; Score 14; DB 1; Length 4; Best Local Similarity 75.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /product= "Lys(BOC)"
OTHER INFORMATION: /note= "N-terminal: FMOC"
FRATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: /product= "Asp(OBut)"
US-08-329-820-88
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US-08-581-918A-17
; Sequence 17, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KAAD 4
                                                                                                                 2 KAMD 5
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Gaps

APPLICANT: Beach, David H

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Gaps
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Beneral No. 6486131

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Demetrick, Douglas J.

APPLICANT: Demetrick, Douglas J.

APPLICANT: Hannon, Gregory J.

TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES

TITLE OF INVENTION: RELATED THERETO

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4;
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                                                                                                        STATE: MA

COUNTRY: USA
ZIP: O02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,214D
FILING DATE: 30-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/26,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PRIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PRIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
ATTONEY, AGENT INFORMATION:
ANALY: VALCOLE MATCHARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.05
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 17:
                 NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 3; Conserv
                                                                           STREET: One E
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APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STARE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Patent No. 6331390
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 14; DB 3; Length 4; 75.0%; Pred. No. 4.1e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KAMD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-346-147B-17
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APPLICANT: Lockhart et al.
APPLICANT: Lockhart et al.
APPLICANT: AFTMERTION: Inc.
TITLE OF INVENTION: Signatures and Methods Involving the Same
TITLE OF INVENTION: Signatures and Methods Involving the Same
TITLE OF INVENTION: Signatures and Methods Involving the Same
TITLE OF INVENTION: Signatures and Methods Involving the Same
CURRENT APPLICATION NUMBER: US/08/933,219B
CURRENT FILING DATE: 1997-09-18
PRIOR PAPLICATION NUMBER: 60/025,740
PRIOR FILING DATE: 1996-09-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATION UNMER: PC COMPATIBLE
APPLICATION UNMER: US/08/528,523
FILING DATE: 06-NOV-1992
CLASSIFICATION NUMBER: BP 94114572.4
APPLICATION NUMBER: BP 94114572.4
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/POCKET NUMBER: Merck 1717
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%; Score 14; DB 2; Length 5;
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      NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-08-933-219B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-933-219B-2; Sequence 2, Application US/08933219B; Patent No. 6329140
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 64191
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 5 amin ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                               CITY: Arlington
                                                                                                                                                        STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KAM 4
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LENGTH: 5
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Pred. No. 4.1e+05;
                                                                                                      COUNTY: UGA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,750C
FILING DATE: 30-JAN-1998
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/93,274
FILING DATE: 15-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 14-APR-1994
RIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 18-NOV-1993
RIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
RIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
RIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 10-OCT-1993
RIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 10-OCT-1993
REPRENCE/DOCKET NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Patent No. 5824782
GENERAL INFORMATION:
APPLICANT: Hoelzer, Wolfgang
APPLICANT: von Hoegen, Ilka
APPLICANT: Strittmatter, Wolfgang
APPLICANT: Marzku, Siegfried
TITLE OF INVENTION: Immunoconjugates II
E: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%;
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                     STREET: One P
CITY: Boston
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      ADDRESSEE:
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                              Gaps
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OTHER INFORMATION: Cyclicized modulating agent comprising
TOTHER INFORMATION: desmoglein-1 cell adhesion recognition sequence
US-09-535-852-1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086,407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT APPLICATION NUMBER: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: PastSEQ for Windows Version 4.0
IENGTH: 5
                                                                                                                                                                            RESULT 14
US-09-321-481-2
Sequence 2, Application US/09321481
Sequence 2, Application US/09321481
Sequence 2, Application US/09321481
Sequence 2, Application US/09321481
Sequence 2, APPLICAMTION:
TITLE OF INVENTION:
TITLE OF INVENTION: Signatures in Nucleic Acid Molecules
FILE REPERENCE: 3016.2
CURRENT FILING DATE: 1999-05-27
CURRENT FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 08/933,219
PRIOR APPLICATION NUMBER: 08/933,219
PRIOR APPLICATION NUMBER: 08/933,219
SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 5
100.0%; Pred. No. 4.1e+05; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%; Score 14; DB 4; Length 5; 50.0%; Pred. No. 4.1e+05; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.3%; Score 14; DB 3; Length 5; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Synthetic Sequence
OTHER INFORMATION: Synthetic Sequence
US-09-321-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-535-852-1028
; Sequence 1028, Application US/09535852
; Patent No. 6638911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Search completed: May 26, 2005, 19:59:55
Job time : 41 secs
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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 20:08:51; Search time 39 Seconds (without alignments) 29.605 Million cell updates/sec

1 LKAMDPTPPLWI 12 US-10-047-945-4 69 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

1582 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 12 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	QI :	Description
-	27	39.1	7	~	A61081	tryptophyllin, bas
7	27	39.1	10	~	A36454	trypsin-modulating
٣	24	34.8	80	7	S21288	lectin - potato (f
4	23	33.3	7	4	A58725	Ë
S	21	30.4	10	7	C35389	urease (EC 3.5.1.5
9	21	30.4	1.0	~	B59272	peptide-N4- (N-acet
7	21	30.4	10	~	S39030	lysyl-bradykinin -
æ	21	30.4	11	٦	XAVIBH	bradykinin-potenti
თ	20	29.0	S	7	B60274	major protein anti
10	20	29.0	80	7	S10783	
11	20	29.0	80	7	A39308	glycine reductase
12	20	29.0	12	٦	JIJG0	tremerogen A-10 -
13	20	6	12	~	PN0663	dystrophin-associa
14	19	•	6	~	B30572	T-cell receptor be
15	19	27.5	σ	7	A60108	exotoxin A - Strep
16	19	27.5	9	7	S26508	collagen alpha 2(V
17	19	27.5	10	7	C30572	T-cell receptor be
18	19	27.5	11	~	D45900	complement C3b rec
19	18	26.1	4	~	151049	metallothionein-A
20	18	26.1	œ	7	S71919	alcohol dehydrogen
21		26.1	10	~	PC2171	triacylglycerol li
22		26.1	10	~	A61007	hementin (EC 3.4
23	18	26.1	11	~	C61497	seed protein ws-18
24		26.1	12	7	A49033	T-cell receptor de
25	18	26.1	12	~	JQ2308	hypothetical 1.4K
56	18		12	~	JQ2318	hypothetical 1.4K
27	18	26.1	12	~	158273	thyroglobulin - ra
28	18	26.1	12	0	S07436	tachykinin - Afric
53	17	24.6	7	~	809652	hypothetical prote

leucokinin VII - M alpha-gliadin 4Ha alpha-dliadin 6Ha	bera-glucosidase (microbial collagen napin small chain	IG H Chain V-D-J r IG H chain V-D-J r ATP Bynthage D Cha lebetin 1 igoform	acid proteinase li adipokinetic hormo acylase – Kluyvera	angiotensin-conver gene c-mpl protein ATPase Rl subunit
JS0317 A61218 B61218	PQ0231 A26093 S70337	PH1587 PH1611 PN0046 S71380	B37988 S10596 S19288	A31570 I58350 D48186
0 0 0	0100	0000	000	000
10 10	122	1222	വ മേ മ	
24.6 24.6	24.6	24.6 24.6 6.6.6	23.2.2	23.2
17	17	17	16 16	16 16 16
30 32	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	9 9 9 9 9 9 8 7 8	4 4 4 0 1 2	4 4 4 6 4 3

ALIGNMENTS

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tryptophyllin, basic - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
A61081
```

C;Accession: A61081

R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.

R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.

R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containi

A;Reference number: A61081

A;Accession: A61081

A Molecule type: protein A; Residues: 1-7 < AMON. C; Comment: The biological activity of this peptide was not determined. C; Superfamily: unassigned animal peptides C; Superfamily: unassigned animal peptides C; Supervise: amidated carboxyl end; hydroxyproline; skin F; 3/Modified site: 4-hydroxyproline (Pro) #status experimental F; 7/Modified site: amidated carboxyl end (Pro) #status experimental

Gaps ö 1; Indels Length 7; Score 27; DB 2; L Pred. No. 2.8e+05; 0; Mismatches 1; Query Match 39.1%; Best Local Similarity 80.0%; Matches 4; Conservative (

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8 PPLWI 12 PPSWI 6 셤 ઠે

trypsin-modulating oostatic factor - yellow fever mosquito

C;Species: Aedes aegypti (yellow fever mosquito) C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004 C; Accession: A36454; A61630

RiBorovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F. PASEB J. 4, 3015-3020, 1990 A;Title: Mosquito osciatic factor: a novel decapeptide modulating trypsin-like enzyme biv A;Reference number: A36454; MUID:90367888; PMID:2394318

A; Accession: A36454

A; Molecule type: protein A; Residues: 1-10 < BOR>

A;Cross-references: UNIPROT:P19425
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A;Reference number: A61630; MUID:93357794; PMID:8353526

A; Accession: A61630

A;Molecule type: protein A;Residues: 1-10 <B02>

A, Note: none of the amino acids is modified C; Function:

A, Description: inhibits systhesis of trypsin- and chymotrypsin-like enzymes by midgut ep

05:58:06 2005

Tue May 31

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Gaps

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R.Hu. L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of ge
A;Reference number: A35389; MUID:90264298; PMID:2345135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain - N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May_2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RiAltmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Bus, J. Blochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:981894; PMID:9523720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Conlon, J.M.; Olson, K.R.
PEBS Lett. 334, 75-78, 1993
A;Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla
A;Reference number: S39030; WUID:94039817; PMID:8224232
                      C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004 C;Accession: C35389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lysyl-bradykinin - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 2; Lengtn 10, Pred. No. 1.28+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule: type: protein
A,Residues: 1-10 <ALT>
A,Cross-references: UNIPROT:P81898
C,Keywords: hydrolase
                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 *HWA.
A;Cross.references: UNIPROT: P17339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: Q9PRZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.4%;
                                                                                                                                                                                                                                                                                                                                                                           30.4%;
  C;Species: Morganella morganii
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Matches 3; Conservative
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Matches 3; Conserv
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                       C; Keywords: hydrolase
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                                                                                                                                                                                     A; Accession: C35389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: B59272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S39030
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Rymilar, D.J.; Allen, AK.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 192-8
A,Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizatio
A,Reference number: S21288; MUD:92272683; PMID:1590771
A,Accession: S21288; MUD:92272683; PMID:1590771
A,Accession: S1288
A,Molecule type: protein
A,Residues: 1-8 <MIL>
A,Residues: 1-8 <MIL>
A,Experimental source: Var. Ulster Sceptre
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R; Faulstch, H.; Buku, A.; Bodenmueller, H.; Wieland, T.
Biochemistry 19, 334-343, 1980
A; Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A; Reference number: A58725; MUID:6893271; PMID:6893271
A; Recession: A58725
A; Status: prellminary
A; Molecule type: procein
A; Residues: 1-7 <FAU>
C; Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide
F; 2/Modified site: D-threonine (Thr) #status experimental
F; 2/Modified site: D-threonine (Thr) #status experimental
F; 3/Modified site: (3R, 45)-3, 4-dihydroxyproline (Pro) #status experimental
F; 6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
F; 7/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
F; 7/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
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                                                                                                                                                                                                                                                                                                                               lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: S21288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virotoxin - destroying angel
C;Species: Amanita virosa (destroying angel)
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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                                                       Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 57.1%; Pred. No. 2.8e+05; Similarity 57.1%; Pred. No. 2.8e+05; 4; Conservative 1; Mismatches 2; Indels
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Pred. No. 2.8e+05;
1; Mismatches 2; Indels
                                                                                                      1; Indels
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                                              39.1%; Score 27; DB 2; I
Similarity 80.0%; Pred. No. 1.2e+02;
4; Conservative 0; Mismatches 1;
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Matches 4; Conserv
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                                                 Query Match
Best Local Similarity
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2 ASTPSPP 8
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                                                                                                                                                             5 DPTPP 9
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C; Keywords: hormone
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J. Biol. Chem. 266, 22147-22153, 1991
A; Title: Glycine reductase protein C. Properties and characterization of its role in th-A; Reference number: A39308; MUID:92042141; PMID:1939235
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tremerogen A-10 - jelly fungus (Tremella mesenterica)
C;Species: Tremella mesenterica
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01642; A61313
R;Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
Science 212, 1525-1527, 1981
A;Title: Peptide sex hormones inducing conjugation tube formation in compatible mating-t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-12 <SAKI>
A;Residues: 1-12 <SAKI>
A;Cross-references: UNIPROT:P01371
A;Cross-references: UNIPROT:P01371
A;Nord stancesyl may instead be (2E,6E,102)-12-hydroxyfarnesyl
R;Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.
Agric. Biol. Chem. 42, 1301-1302, 1978
A;Title: Amino acid sequence of tremerogen A-10, a peptidal hormone, inducing conjugatic
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C;Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; pheror
F;12/Binding site: farnesyl (Cys) (covalent) #status experimental
F;12/Modified site: methyl ester carboxyl end (Cys) #status experimental
                                                                                                                                                                                                                                                                   sulfhydryl protein C, alpha chain - Clostridium stickla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: glycine reductase complex catalyzes the reductive deamination of glycine C; Keywords: ATP; oxidoreductase
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C;Comment: Tremerogen A-10 is produced by the A mating-type cells and induces formation
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                                                                                                                                                                                                                                                       glycine reductase (EC 1.4.99.-) sulfhydryl protein C, alpha chain - Clostri
C;Species: Clostridium sticklandii
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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Stadtman, T.C.; Davis, J.N.
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A; Molecule type: protein
A; Residues: 1-11 < CHI>
A; Residues: 1-11 < CHIP < CHIP
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major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

Cispecies: Mycobacterium tuberculosis

Cispecies: Mycobacterium tuberculosis

Cispecies: Mycobacterium tuberculosis

Cibate: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

Cibate: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

Cibate: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

Rivagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Rivagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Riveference number: A60274; MUD:91099989; PMID:1898899

A;Accession: Bocota

A;Accession: Bocota

A;Residues: protein

A;Residues: 1-5 <NAG>
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: $10783
C;Accession: $10783
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A;Accession: $10783
A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein
                                                                                                                                                                   C;Species: Agkistrodon halys (halys viper)
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Date: 30-Sep-1986 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Date: 30-Sep-1986 #sequence_revision 30-Sep-1988 #text_chang, W.D.
R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
Peptides 6, 339-342, 1985
A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese A;Reference number: JC0002; MUID: 86177022; PMID: 3008123
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0
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Pred. No. 1.3e+03;
1; Mismatches 1; Indels
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                                                                                                   bradykinin-potentiating peptide - halys viper
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                               Alternate names: BPP
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Search completed: May 26, 2005, 20:18:24 Job time : 41 secs
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0663
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Yitle: A dystrophin-associated glycoprotein, Ala (one of 43DAG doublets), is retained A;Reference number: PN0662; MUID:94156881; PMID:8113213
A;Rocession: PN0663
A;Rocession: PN0663
A;Rocession: I-12 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: glycoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             July 1 receptor beta chain C region (CRTB29) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C;Accession: 131057-1035, 1989
July 111ams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989
A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz A;Reference number: A30563; MUID:89110038; PMID:2563271
A;Reference number: A30563; MUID:89110038; PMID:2563271
A;Reference number: A30563; MUID:89110038; PMID:263271
A;Reference number: A30563; MID:89110038; PMID:263271
C;Keywords: T-cell receptor
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NyAlternate names: blastogen A; scarlet fever toxin
C;Species: Streptococcus pyogenes
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60108
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Best Local Similarity
Matches 3; Conserv
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Gaps

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5 DPTP 8 DPDP 5

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GenCore version 5.1.6
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                    Copyright
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protein search, using sw model ı OM protein Run on:

May 26, 2005, 20:00:51; Search time 171 Seconds (without alignments) 35.935 Million cell updates/sec

US-10-047-945-4

1 LKAMDPTPPLWI 12 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

4233 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 12 88 Minimum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	1	Description	P83455 pachymedusa	P19425 aedes aegyp	homo		Q8kz86 acinetobact	Q7mlv6 solanum tub	Q76mk5 eurypharynx	Q8ivg8 homo sapien				Q8mb58 seddera hir	Q8mb77 odonellia h	Q8mb79 aniseia arg	merremi	Q8mbel ipomoea alb		Q9h326 homo sapien	Q6sp94 chlamydomon			_		P17339 morganella		P04562 agkistrodon	077896 oreochromis	Q47251 escherichia			Q91wz3 rattus sp.
SUMMAKIES	f	21	TPFY_PACDA	TMOF_AEDAE	Q9UCR1	Q6X7V1	Q8KZ86	Q7M1V6	Q76MK5	Q8IVG8	Q8MAZ1	Q8MAZ3	Q8MB39	Q8MB58	Q8MB77	Q8MB79	Q8MB97	Q8MBE1	EI01_LITRU	09н326	Q6SP94	099193	Q9PRJ4	BRK_ONCMY	PNAS_PRUDU	URE3 MORMO	Q67BK2	BPP_AGKHP	077896	047251	UF04 MOUSE	Q7M0L0	Q91WZ3
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	Query	March	39.1	39.1	37.7	36.2	36.2	34.8	33.3	33.3	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	29.0	29.0	29.0
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Q75595 human immun Q9hcn5 homo sapien	P01371 tremella me Q9bz49 homo sapien		Q9et16 mesocricetu	Q9et17 mus caroii Q9et18 mus spretus	Q7m2m9 bos taurus P83278 macrobrachi	P40930 homo sapien	Q8vhm9 mus musculu	Q9esu5 mus musculu
Q75595 Q9HCN5	TA10_TREME Q9BZ49	Q7YNG6 Q6ldp8	09ET16	Q9ET18	Q7M2M9 FAR5 MACRS	UHA3_HUMAN	Q8VHM9	Q9ESU5
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33	34 35	36 37	38	2. A. V. O.	4 4 2 2	43	44	45

ALIGNMENTS

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GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
Amidation; Amphibian defense peptide; Direct protein sequencing;
                                                                                                                                                                                                  [1] -
SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                           CDNA.";
Submitted (SEP-2002) to Swiss-Prot.
-!- FUNCTION: Mycactive. Has selective relaxing activity on vascular smooth muscle.
smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                             TISSUE=Skin secretion;
Chen T.B., Orr D.F., Shaw C.;
"Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural
characterization, pharmacological activity and cloning of precursor
                                                                                        Trypcophyllin-1 (Pdr-1).

Pachymedusa dacnicolor (Glant mexican leaf frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea; Hylidae; Phyllomeduainae, Pachymedusa.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Trypsin-modulating obstatic factor (TMOF) (OOSH).
Aedes aegypti (Yellowfever mosquito).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7;
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7 7 Proline amide.
7 AA; 794 MW; 7772D37DC7776350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.1%; Score 27; DB 1; 1 60.0%; Pred. No. 1.6e+06; tive 1; Mismatches 1;
                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                  7 AA.
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                    PRT;
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Best Local Similarity 60.0
Matches 3; Conservative
                    STANDARD;
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                TPFY PACDA P83455;
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P19425;
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MOD_RES
SEQUENCE
TWOF AEDAE

ID TWOP AE

AC P19425,

DT 01-NOV.

DT 25-CCT.

DZ 25-CCT.

DS Aedes i

OC Bukary
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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDILINE=22929740; PubMed=12890727; Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.; Isolation and expression analysis of the canine insulin-like factor 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22270987; PubMed=12384388; Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin E., Monti-Bragadin C., Lavenia A., Dolzani L.; Monti-Bragadin C., Lavenia A., Dolzani L.; "Molecular characterization of integrons in epidemiologically unrelated clinical isolates of Acinetobacter baumannii from Italian hospitals reveals a limited Ddversity of gene cassette arrays."; Antimicrob. Agente Chemother. 46:3665-3668 (2002).

EMBL, AJ31334; CAC65941.1; -.
                                                                                                                                                                                                                                           Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Moraxellaceae, Acinetobacter.
NCBI_TaxID=470;
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                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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, Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last seq
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01-MAR-2004 (TrEMBLrel. 26, Created)
                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene.";
Biol. Reprod. 69:1658-1664(2003).
EMBL; AY251015; AAP79619.1; --
NON TER 12 12
                                                                                                                                                                                      Insulin-like factor 3 (Fragment).
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                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                              Q6X7V1;
05-JUL-2004
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                                                                                                     STRAIN=Vero beach; TISSUE=Covary;
MEDLINE=90367888; PubMed=2394318;
Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
"Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme biosynthesis in the midgut.";
PASEB J. 4:3015-3020(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development.
--- DEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs and stops at 56 hrs.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=92129337; PubMed=1733949;
SETACKE M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V., Stracke M.L., Liutea L.A.;
Schiffmann E., Liotta L.A.;
"Identification, purification, and partial sequence analysis of autocaxin, a novel motility-stimulating protein.";
J. Biol. Chem. 267:2524-2529(1992).
Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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Pred. No. 9.7e+02;
0; Mismatches 1; Indels
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Direct protein sequencing; Hormone.

DOMAIN

3 10 Poly-Pro.

1 2 YD -> DY (in TMOF(B)).

1 1 2 YD -> DY (in TMOF(B)).
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
AUTOTAXIN (Fragment).
Homo Sapiens (Human).
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity
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                   NCBI_TaxID=7159
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Bukaryotta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamida, Solanales, Convolvulaceae, Maripeae, Maripa.
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"Monophyly of the Convolvulaceae and circumscription of their major
lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522 (2002).
EMBL; AX100937; AAM55669.1; -.
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                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
05-ULL-2004 (TrEMBLrel. 27, Last annotation update)
Low density lipoprotein receptor related protein I (Lipoprotein receptor related protein)
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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BMB1, Y18524; CAD57169.1; --
EMB1, X18524; CAD33464.1; --
GO, GO:0004872; F:receptor activity; IEA.
Lipoprotein; Receptor.
NON TREES TO THE SEQUENCE TO THE SEQUENCE
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MEDLINE=90089395; Pubmed=2597675;
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                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                         Lectin (Fragment).
Solanum tuberosum (Potato).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids, Solanales; Solanaceae, Solanum.
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Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
                                                                                                                                                                                                                                                                                                                               Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R., Bolwell G.P.,
"Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
Characterization, immunolocalization and effects of wounding.";
Biochem. J. 283:813-821(1992).
PIR; S21288; S21288.
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Pred. No. 4.3e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.8%; Score 24; DB 2; Length 8; 57.1%; Pred. No. 1.6e+06; ive 1; Mismatches 2; Indels
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10 AA; 1217 MW; D99C5E75A76AA736 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA; 771 MW; C37775A771B5BDDA CRC64;
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Mitochondrion.
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Name=ATPase 8;
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3; Conservative
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RESULT 7

Q76MK5

D0 Q76MK6

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D1 O5-J0

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D1 O5-J0

D2 O5-J0

D3 O5-J0

D4 O5-J0

D7 O5-J0

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Seddera hírsuta.
Chloroplast.
Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Convolvulaceae; Cresseae; Seddera.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Convolvulaceae; Anisieae; Odonellia.
                                                                                                                                                                                                                                                                                                                                                                            Stefanovic S., Krueger L., Olmstead R.G.;
"Monophyly of the Convolvulaceae and circumscription of their mulineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522(2002).
EMBL; AX100905; AAM55743.1; -.
GO; GO:000557; C:chloroplast; IEA.
Chloroplast.
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EMBL, AX100897; AAMS5711.1; -.

GO, GO:0009507; C:chloroplast; IEA.
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100.0%; Pred. No. 6.9e+03;
tive 0; Mismatches 0;
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(TrEMBLrel. 24, I
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(TrEMBLrel. 22, I
(TrEMBLrel. 24, I
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Convolvulaceae; Cresseae; Wilsonia.
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"Monophyly of the Convolvulaceae and circumscription of their major lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522(2002).
EMBL; AX100936; AAM55665.1; -.
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"Monophyly of the Convolvulaceae and circumscription of their major
lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522 (2002).
EMBL; AY100914; AAM55777.; --
GO; GO:0009507; C:chloroplast; IEA.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Convolvulaceae, Anisieae, Aniseia.
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Stefanovic S., Krueger L., Olmstead R.G.;
"Monophyly of the Convolvulaceae and circumscription of their major lineages based on DAN sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522(2002).
EMBL; AX100895; AAM55703.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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Stefanovic S., Krueger L., Olmstead R.G.;
"Monophyly of the Convolvulaceae and circumscription of their major lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522 (2002).
EMBL; AX100885; AAM55663.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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SEQÜENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;
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Best Local Similarity
Matches 3; Conserv
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Merremia peltata.
Chloroplast.
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Q8MB79
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Oy 9 PLW 11

Db 9 PLW 11
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Search completed: May 26, 2005, 20:17:51 Job time : 185 secs

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protein search, using sw model OM protein

May 26, 2005, 20:00:02; Search time 159 Seconds (without alignments) 29:189 Million cell updates/sec Run on:

US-10-047-945-4 69

1 LKAMDPTPPLWI 12 score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

520583 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 12 88 Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp20028:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	uc.	Synthetic	Synthetic	N-terminu	Synthetic	Synthetic	Synthetic	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Hydroxyme	Human can	Human can	Human can	Human 213	Human can	Human can	Нитап сап	Human can
	Description	Abb80225	Abb80226	Aaw53843]	Abb80222	Abb80227	Abb80228	Abr12621 1		Abr12854 1	Abr12743 1	Abr11875 1	Abr12121 1		Abr12106 1		Abr12738 1	Aaw21252]	Abr11778 1	Abr12206 1	Abr12924 1	Ado64358 1	Abr12770 1	Abr12969 1		Abr12601
	A	ABB80225	ABB80226	AAW53843	ABB80222	ABB80227	ABB80228	ABR12621	ABR12017	ABR12854	ABR12743	ABR11875	ABR12121	ABR12948	ABR12106	ABR12294	ABR12738	AAW21252	ABR11778	ABR12206	ABR12924	AD064358	ABR12770	ABR12969	ABR12458	ABR12601
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	Match	100.0	94.2	78.3	78.3	72.5	62.3	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	55.1	53.6	53.6	53.6	53.6	52.2	52.2	52.2	52.2
	Score	69	65	54	54	20	43	41	41	41	41	41	41	41	41	41	41	38	37	37	37	37	36	36	36	36
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ABR12046 ABR12234 AD072233 AD072483 AD0724664 AD0725664 AD072536 AD065216 AD067338 AD067338 AD067338 AD0673238 AD0673238 AD0673238 AD0673238 AD0677387 AD0677387 AD0677387 AD0677387 AD0677387 AD0677387 AD0677387 AD0677387	
	
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ALIGNMENTS

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA. ABB80225 standard; peptide; 12 AA. (first entry) Synthetic LTNF, LT-12. 06-NOV-2003 ABB80225; ABB80225

Synthetic.

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WO2003060471-A2

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

e.g. Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

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arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifuged immediately, whereas blood requires can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lethal toxin neutralising factor; LINF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematoses (BLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Garaves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by
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                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                   100.0%; Score 69; DB 7; Length 12; 100.0%; Pred. No. 0.00033; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80226 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 4; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                        1 LKAMDPTPPLWI 12
                                                                                                                                                                                                                                                                                                                                                                                              1 LKAMDPTPPLWI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic LTNF, LT-11.
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                                                                                                                                                                                                                                 Sequence 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy, anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                              Length 11;
                                                                                                                                                                            Score 65; DB 7; I
Pred. No. 0.0013;
                                                                                                                                                                   94.2%; Sco...
100.0%; Pred. No. v...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00058387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                              11; Conservative
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                                                                                                                                                                                                                                                                           1 LKAMDPTPPLW 11
                                                                                                                                                                                                                                                  1 LKAMDPTPPLW
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Б. Х.
                                                                                                                                                                                              Local Similarity
                                                                                                                                              Sequence 11 AA;
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(LIPP/) LIPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1994;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), insive growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, at disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins
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                                                                                                                                                                                                                                                                                                                           Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogran's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , whereas an assay of proteins from
                                       Gaps
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     Length 10;
                                     0; Indels
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   Score 54; DB 2;
Pred. No. 0.067;
0; Mismatches 0
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   78.35,
100.08; Pr.
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                                                                                                                                                                                                                                                             (first entry)
                                       Conservative
                                                                       10
                                                                                          LKAMDPTPPL 10
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Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    saliva; ELISA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                             ABB80222;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & [1g5], nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Adisease or Hodgkin's disease) or depression: The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of perform saliva can be centrifuged immediately, whereas blood requires
                                                                                                                                                                                                                                                                                 Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 10g; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLB; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                              ABB80227 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-2003; 2003WO-US001044.
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                                                                                                                                                                                                          06-NOV-2003 (first entry)
10
                   1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                 Synthetic LTNF, LT-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipps BV, Lipps FW;
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                                                                                                                                                                                                                                                                                                                                                                                    saliva; ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                      ABB80227;
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                                                                                                                                                                                                                                                                                                                                                                  Graves'
                                                                                                                ABB80227
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Gaps

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72.5%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels

Conservative

1 LKAMDPTPP

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Gaps ö

78.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.067; ive 0; Mismatches 0; Indels

10; Conservative

Query Match Best Local Similarity Matches 10; Conserva

Query Match Best Local Similarity Matches 9; Conserv

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Human cancer-related protein 156P1D4 HLA peptide #856.
                                       ABR12621 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2002; 2002WO-US011654
                                                                                                                    19-MAY-2003 (first entry)
                                                                                                                                                                                                 Human; cytostatic; vacci
human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                  WO200283921-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jakobovits A,
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          24-OCT-2002.
                                                                              ABR12621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                    ABR12621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in ABB80222-28 represent lethal toxin neutralising factor (ICMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IGE), insuria, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, asthma, diabetes, autoimmune disease (a.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins and the elevating time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1gE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.3%; Score 43; DB 7; Length 8; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                 ABB80228 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2003; 2003WO-US001044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-2002; 2002US-00047945
                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                   Synthetic LTNF, LT-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-636703/60
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Best Local Similarity
Matches 8; Conserv
1 LKAMDPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003060471-A2
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                                                                                                                                                                                                                                                                                                                                          Graves' diseas
saliva; ELISA.
                                                                                                                                                                                06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                       ABB80228;
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Hubert RS;

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Faris M,

Challita-Eid PM,

vaccine; cancer; immune response; HLA;

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                                                                                                                    New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
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Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                               Claim 13; Page 238; 1021pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR12017 standard; peptide; 9 AA.
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                                                             WPI; 2003-075555/07.
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1 MDPSVPIWI
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                                                                                                                                                                                                                  cancer patients.
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   Morrison K,
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ID ABR:
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AC ABR:
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DT 19-1
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1 LKAMDPTP 8

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ABR12743;
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                                                                                                                                                                                                                                                                                               The present invention relates to novel human cancer-related genes and proteins (ABZ70120-ABZ70186 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and poptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present effects is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                           New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                           W, Hubert RS;
Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 6; Length 9; Pred. No. 1.8e+06; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytostatic; vaccine; cancer; immune response; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer-related protein 156P1D4 HLA peptide #1089.
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Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                              Claim 13; Page 232; 1021pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR12854 standard; peptide; 9 AA.
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                                                                                         10-APR-2002; 2002WO-US011654.
                                                                                                              10-APR-2001; 2001US-0282739P.
                                                                                                                       10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human leukocyte antigen.
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                                                                                                                                                      (AGEN-) AGENSYS INC.
                                                                                                                                                                                                       WPI; 2003-075555/07
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Best Local Similarity
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MDPSVPIWI
                                                                                                                                                                                                                                                                                                                                                                                                                  from the inventior
                                                                                                                                                                                                                                                           cancer patients.
                                                  WO200283921-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                              Homo sapiens
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                                                                      24-OCT-2002
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                                                                                                                                                                 proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                    modulates the structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                Ge ₩,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.4%; Score 41; DB 6; I 66.7%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                    composition comprising a substance that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                   Faris M,
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Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                , Challita-Bid PM, Faris
Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 240; 1021pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR12743 standard; peptide; 10 AA
10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                       (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                cancer patients.
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                                                                                                                                                                                Jakobovits A,
                                                                                                                                                                                                                   Morrison K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
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                                                                                                        proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
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                                                                                                                                                                                                                                                                                                               The present invention relates to novel human cancer-related genes and
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                                                                            composition comprising a substance that modulates the structure
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Pred. No. 7.9;
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                                                                                                                                                                                                                                         Claim 13; Page 239; 1021pp; English.
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25-APR-2001; 2001US-0286630P.
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Matches 6; Conservative
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      WPI; 2003-075555/07
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                                                                                                                                                                          cancer patients
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The present invention relates to novel human cancer-related genes and

Claim 13; Page 231; 1021pp; English.

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The genes are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                                                                                                                                                                                                                                      Score 41; DB (
Pred. No. 7.9;
2; Mismatches
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Morrison K, Morrison RK, Raitano AB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR12121 standard; peptide; 10
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                                                                                6; Conservative
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MDPSVPIWI
                                                                                                                                                                                          from the invention
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Best Local Similarity
Matches 6; Conser
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vaccine; cancer; immune response; HLA;

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New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                   Human cancer-related protein 156P1D4 HLA peptide #341.
                                                                    ABR12106 standard; peptide; 10 AA.
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25-APR-2001; 2001US-0286630P.
                                                                                                                          19-MAY-2003 (first entry)
                                                                                                                                                                                             human leukocyte antigen.
    1 MDPSVPIWI 9
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                                                                                                                                                                                                                                                                                                                                                                                       (AGEN-) AGENSYS INC.
                                                                                                                                                                                cytostatic;
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Morrison K, 1
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                                                                                               ABR12106;
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                                                                                                                                                                                 Human;
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Matches
                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the structure of proteins and polynuclectides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                    Human; cytostatic; vaccine; cancer; immune response; HLA;
                                                       6; Length 10;
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                                                                                                                                                                                                                                                                                         Human cancer-related protein 156P1D4 HLA peptide #1183.
                                             59.4%; Scor.
66.7%; Pred. No. /...
2; Mismatches
                                                       Score 41; DB 6
Pred. No. 7.9;
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Morrison K, Morrison RK, Raitano AB;
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                                                                                                                                                                                                        ABR12948 standard; peptide; 10 AA.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                             (first entry)
                                                                                 6; Conservative
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MDPSVPIWI 9
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                                                    Query Match
Best Local Similarity
Matches 6; Conserv
from the invention
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                             Sequence 10 AA;
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ABR12948
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Ge ₩,

Faris M,

, Challita-Eid PM, Faris Morrison RK, Raitano AB;

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The present invention relates to novel human cancer-related genes and proteins (ABZ79120-ABZ79168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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66.7%; Pred. No. 7.9;
iive 2; Mismatches 1
Claim 13; Page 233; 1021pp; English.
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Gaps

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4 MDPTPPLWI 12

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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or callular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic genes. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition.comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
                                                                                                                                                                                                                                                                                                                                                                 Hubert RS;
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                                                   Human, cytostatic, vaccine, cancer; immune response; HLA; human leukocyte antigen.
                  Human cancer-related protein 156P1D4 HLA peptide #529.
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Morrison K, Morrison RK, Raitano AB;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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Matches 6; Conserv
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                                                                                                           Homo sapiens.
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Gaps ö

6; Conservative

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/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1462099 seqs, 344972447 residues
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query

No. Score Match Length DB ID

1 69 100.0 12 14 US-10-047-945-4

2 65 94.2 11 14 US-10-047-945-5

3 54 78.3 10 14 US-10-047-945-5

5 43 62.3 8 14 US-10-047-945-6

5 38 55.1 9 17 US-10-047-945-7

5 43 62.3 8 14 US-10-047-945-7

6 38 55.1 9 17 US-10-930-300-52

8 32 46.4 12 14 US-10-185-815-6

9 32 46.4 12 14 US-10-185-815-6

9 32 46.4 12 15 US-10-185-815-6

9 34 46.4 12 15 US-10-16-791-252

11 31 44.9 9 16 US-10-16-198

Sequence 52, Application of Applica

	sequence 619, Apple Sequence 619, Apple Sequence 119, Apple Sequence 118, Apple Sequence 273, Apple Sequence 273, Apple Sequence 136, Apple Sequence 116, Apple Sequence 20, Apple Sequence 20, Apple Sequence 23, Apple Sequence 23, Apple Sequence 24, Apple Sequence 25, Apple Sequence 26, Apple Seque
US-10-190-082-480 US-10-437-708-165 US-10-418-032-165 US-10-25-567A-2288 US-10-257-292-7 US-10-277-292-7 US-10-277-292-7 US-10-057-475B-10870 US-10-057-475B-10870 US-10-057-475B-10870 US-10-154-884B-10870 US-10-154-884B-10870 US-10-154-884B-10929 US-10-154-884B-10929 US-09-935-430-74	US-10-277-228-6 US-110-280-340-6 US-110-280-340-6 US-110-285-175-1 US-10-235-175-1 US-08-344-824-38 US-08-739-822-7 US-08-739-822-7 US-09-739-822-7 US-09-758-128-20 US-09-758-128-20 US-09-758-128-20 US-09-758-128-20 US-09-758-128-20
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ALIGNMENTS

US-10-047-945-4

1 US-10-047-945-4

1 Sequence 4, Application US/10047945

1 Publication No. US2003015755A1

1 GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, BINIE V.

TITLE OF INVENTION: [1GE) IMPLICATED DISORDERS

TITLE OF INVENTION: USA010-0505

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT APPLICATION NUMBER: US/10/047,945

FRIOR FILING DATE: 2002-01-14

PRIOR FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US/10/047,945

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 4

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE: NAME/KEY:

LOCATION:

LOCATION:

OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.

US-10-047-945-4

OURLY MARCH:

DOUGHY MARCH:

HIMILIATILY 100.0%; Score 69; DB 14; Length 12;

Guery Match 12; Conservative 0; Mismatches 0; Indels 0; Gaps

OV 1 LEXAMDPTPPLM! 12

DD 1 LEXAMDPTPPLM! 12

RESULT 2

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| Publication No. US20030157555A1
| Publication No. US20030157555A1
| GENERAL INFORMATION: | GENERAL INFORMATION: |
| APPLICANT: LIPPS, BINIE V. |
| APPLICANT: LIPPS, REDERICK W. |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E |
| TITLE OF INVENTION: USPENDING TO SERVICE FOR EACH OF SERVICE FOR IMMUNOGLOBULIN E |
| FILE REFERENCE: FMLPATO15US |
| CURRENT APPLICATION NUMBER: US/10/047,945 |
| PRIOR PILING DATE: 2002-01-14 |
| PRIOR PILING DATE: PRIOR FILING DATE: |
| NUMBER OF SEQ ID NOS: 7 |
| SOFTHARE: WORDPERFECT 5.1 FOR WINDOWS
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION:
TITLE OF INVENTION: (198) IMPLICATED DISORDERS
FILE REFERENCE: FREDRICKE WI.
TITLE OF INVENTION: (198) IMPLICATED DISORDERS
FILE REFERENCE: FRIPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOSTWARE: WORDPERFECT 5.1 FOR WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.5%; Score 50; DB 14; Length 9; 100.0%; Pred. No. 1.3e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:

OTHER INFORMATION: Synthetic.

US-10-047-945-7
                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic.
                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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LKAMDPTP 8
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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LOCATION:
                                                                                                                                                                                                                                                                                     SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corresponds to fragment 1-11 of 2 above.
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US-10-047-945-5

Sequence 5, Application US/10047945

PUBLication No. US20030157555A1

GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIGGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

PRIOR FILING DATE:
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Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOCIOBULIN JITLE OF INVENTION: QUENTION: US/10/047,945
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE: 2002-01-14
PRIOR FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 10; 0.15;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
LENGTH: 10
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 5
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.2%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic.
US-10-047-945-5
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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Gaps
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APPLICANT: Elan Corporation, plc
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
FILE REFERENCE: E1067-20093
CURRENT APPLICATION NUMBER: US/10/185,815
CURRENT FILING DATE: 2001-00-09
PRIOR APPLICATION NUMBER: 60/302,591
PRIOR PRING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OUILIAM, Lawrence A.
APPLICANT: POWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.4%; Score 32; DB 14; Length 12; 100.0%; Pred. No. 3.5e+02; rative 0; Mismatches 0; Indels
    Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
         ;
      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: polypeptide ligand US-10-185-815-6
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APPLICATION NUMBER: US/10/161,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 252, Application US/10161791; Publication No. US20030186863A1; GENERAL INFORMATION: APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                               Sequence 6, Application US/10185815
Publication No. US20030096354A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
      5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
U.S.A.
                                                 2 KAMDPTPP
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1 QSFDPTPP
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STATE: New York
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 12
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    Matches
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Publication No. US20040181039A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guo, Honliang
APPLICANT: Alyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FILING DATE: 2002-12-20
PRIOR PAPLICATON NUMBER: US/10/327,598
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SEQ ID NO 735
LENGTH: 12
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TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY Disk, 3.50 inch, 1.44MB Storage MEDIUM TYPE: ROPYTIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MS WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-Aug-2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
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85.7%; Pred. No. 1.3e+06;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 16;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,248
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
REGISTRATION NUMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 Colorado Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDENESS: single
STRANDENESS: linear
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-322-737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-322-7389
INPORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.3%;
                                          NUMBER OF SEQUENCES: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: canis familiaris;
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Best Local Similarity 85.7.
                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 DPTPPLW 11
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Best Local Similarity
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US-10-327-598-735
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APPLICANT: Singh-Sandhu, Devender
APPLICANT: Oomen, Raymond P
APPLICANT: Oomen, Raymond P
APPLICANT: Oomen, Raymond P
APPLICANT: Oomen, Raymond P
TITLE OF INVENTION: Tumor Antigens BFA4 and BCY1 for Prevention and/or Treatment of
TITLE OF INVENTION: Cancer
FILE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US 60/394,346
FRICR APPLICATION NUMBER: US 60/394,503
FRICR APPLICATION NUMBER: US 60/394,503
FRICR APPLICATION NUMBER: US 60/411,833
FRICR FILING DATE: 2002-07-09
FRICR FILING DATE: 2002-09-18
FRICR FILING DATE: 2002-09-18
FRICR FILING DATE: 2002-06-60
FRICR FILING DATE: 2002-09-18
FRICR FILING DATE: 2002-06-18
FRICR FILING DATE: 2002-06-18
FRICR FILING DATE: 2002-09-18
FRICR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kieliszewski, Marcia
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gume and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/10/437,708
CURRENT FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US/09/547,693
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin Version 3.0
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (3)..(4); OTHER INFORMATION: The Proline at these positions is a hydroxyproline. US-10-437-708-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
43.5%; Score 30; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 9;
1.3e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 168, Application US/10437708
Publication No. US20040009555A1
GENERAL INFORMATION:
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OTHER INFORMATION: Synthetic
PEATURE:
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ORGANISM: Artificial/Unknown
FEATURE:
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; OTHER INFORMATION: CLP-2825
US-10-611-440-188
              Radvanyi, Laszlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial
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2 ETSPPLW 8
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US-10-116-275-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 52, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Lambkin, Imelia
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Compositions Targeting Peyer's Patches and M Cells and Methods and TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%; Score 32; DB 14; Length 12; 66.7%; Pred. No. 3.5e+02;
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CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SSOFTWARE: Patentin version 3.1
LENGTH: 12
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-196
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
REPERSNEW/COCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEPA: (212) 790-9090
TELEFA: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acids
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Publication No. US20040197912A1
GENERAL INFORMATION:
APPLICANT: Berinstein, Neil
APPLICANT: Gallichan, Scott
APPLICANT: Parrington, Mark
APPLICANT: Parrington, Mark
APPLICANT: Parrington, Mark
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-10-161-791-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KAMDPTPPL 10
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US-10-611-440-188
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Sequence 165, Application US/10437708
Publication No. US20040009555A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT PILING DATE: 2003-05-14
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 165
LENGTH: 10
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CTHER INFORMATION: The Proline at these positions is a hydroxyproline US-10-437-708-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(1) OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 43.5%; Score 30; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
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                                                                                                                                                               Sequence 168, Application US/10418032
Publication No. US20050074838A1
GENERAL INFORMATION:
APPLICANT: Kieliazewaki, Marcia J.
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
TIT
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1 LOCATION: (3)...(4)
2 OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-418-032-168
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LOCATION: (1)._(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.5%; Score 30; DB 17; Length 8; 100.0%; Pred. No. 1.3e+06; rive 0; Mismatches 0; Indels
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Sequence 480, Application US/10190082

Publication No. US20030148264A1

GENERAL INPORMATION:

APPLICANT: Laidu, Sachdev S.

APPLICANT: Aldu, Heike A.

TITLE OF INVENTION: PHACE DISPLAYED PDZ DOWAIN LIGANDS

FILE REFERENCE: P1905R1

CURRENT FILING DATE: 2002-07-03

PRIOR FILING DATE: 2001-07-06

NUMBER OF SEQ ID NOS: 683

SEQ ID NO 480

LENGTH: 10
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ORGANISM: Artificial sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic US-10-190-082-480
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserva
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PTPPL 5
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                                                                                                                                                        US-10-418-032-168
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Gaps

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MOLECULE TYPE: PEPTIDE IN SEQ ID NO: HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE: TEALL
COUNTRY: USA
77401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            US-08-657-163A-2
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18, Appli
7, Appli
7, Appli
2, Appli
2, Appli
2, Appli
12, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                 May 26, 2005, 20:09:44; Search time 40 Seconds (without alignments) 22.395 Million cell updates/sec
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| /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-336-3437.31
US-08-652-877-31
US-08-662-999A-252
US-09-500-124-252
US-09-500-124-252
US-09-547-693-168
US-09-547-693-168
US-09-315-926A-18
US-09-315-926A-18
US-09-315-926A-18
US-09-33-416-7
US-09-33-41-7
US-09-33-41-7
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US-09-295-96B-12
US-09-295-96B-12
US-09-295-946B-12
US-09-295-946B-12
US-09-295-946B-12
US-09-295-946B-12
US-09-295-946B-12
US-09-295-946B-12
US-09-295-946B-12
US-09-551-73RB-12
US-09-551-73B-12
US-09-551-74B-12
US-09-551-74B-12
US-09-551-74B-12
US-09-551-74B-12
US-09-551-74B-12
US-09-551-74B-12
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US-09-551-737C-16
US-09-295-924B-3
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95-996B-13
                                                                                                                                                                                                                                                  513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                          1 LKAMDPTPPLWI 12
                                                                                                                                            US-10-047-945-4
69
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                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 12
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Match 1
                                                                                                                                                               Perfect score:
                                                                                                                                                                                                        Scoring table:
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Maximum DB
                                                          OM protein
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                                                                                       Run on:
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Appli
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                                                         Sequence 4, Ag
Sequence 14, P
Sequence 17, P
Sequence 17, P
Sequence 4, Ag
                                                                                                                                                                                         Sequence 11, 1
Sequence 11, 1
Sequence 7, Ap
                                                                                                                                                      Sequence 14
Sequence 8,
                         Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08657163A

| Sequence 2, Application US/08657163A
| Patent No. 574449
| GENERAL INFORMATION:
| TITLE NO. INVERTION: EMBODIMENTS OF NATURAL AND
| TITLE OF INVERTION: SYNTHETIC LINES AND THEIR
| TITLE OF INVERTION: UTILITY AS TREATMENT FOR ENVENOMATION NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESS: ADDRESSES: BINIE V. LIPPS
| STREET: 4509 MIMOSA DR.
US-09-551-738B-13

US-07-989-290-4

US-08-468-596-4

US-09-295-996B-14

US-09-295-948-17

US-09-251-737C-17

US-09-551-738B-14

US-09-551-738B-14

US-09-295-946B-11

US-09-295-946B-11

US-09-295-946B-11

US-09-551-738B-8

US-09-551-738B-8

US-09-551-738B-8

US-09-551-738B-8

US-09-393-941-3

US-09-393-941-3

US-09-393-941-3

US-09-393-941-3

US-08-178-777-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAPPTER FALDABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION TONER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION SER 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION SER 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: 28,198
REFERENCE/DOCKET NUMBER: 28,198
REFERENCE/DOCKET NUMBER: 13-482-2961
TELEFRAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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STRANDEDNESS
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US-08-476-515A-31
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 APPLICANT:
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                                  Length 10;
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                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                Query Match 78.3%; Score 54; DB 1; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 10; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COLUZI, LAURA A.
REGISTRATION NUMBER: 30,742
REPERBNCE/DOCKET NUMBER: 7683-065
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                US-08-336-341A-31
; Sequence 31, Application US/08336343A
; Patent No. 5677144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION.
APPLICANT: APPLICANT: Juhlin, Claes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akeretrom, Goran
Juhlin, Claes
Rask, Lars
Crumley, Gregg R.
Morse, Clarence C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.4%;
SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                               1 LKAMDPTPPL 10
                                                                                                    1 LKAMDPTPPL 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-336-343A-31
  ; ORIGINAL SUL
US-08-657-163A-2
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-652-877-31
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Gaps
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APPLICANT: Akerstron, Goran
APPLICANT: Akerstron, Claes
APPLICANT: Crumley, Greeg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Hyalm, Goran
APPLICANT: Hyalm, Goran
TILLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
CORRESPONDENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Martin Savitzky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments TITLE OF INVENTION: Thereof and DNA Encoding Same NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.4%; Score 32; DB 3; Length 11; Best Local Similarity 66.7%; Pred. No. 43; Matches 6; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY AREATORY INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELEPHONE: 610-454-3816
                                                                                                                                                                                                                                                                                                SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 31, Application US/08476515A; Patent No. 6239270
                                                                                                                                                                 STATE: PA SOCIATE STATE: PA COUNTRY: USA ZIP: 19426-0107 COMPUTER READABLE FORM: COMPUTER: Macintosh OPERATING SYSTEM: System 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 11 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
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Gaps
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Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: PORL, Channing J.
APPLICANT: PORL, Channing J.
APPLICANT: BER, Channing J.
APPLICANT: BIR, James B.
ITILE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                               MEDIUM 11FE: FLODEY WILLS.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHWER: Patentin Release #1.0, Version #1.30
CNGTWARE: Patentin Release #1.0, Version #1.30
CNGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-196
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistorck, S. Leelie
REGISTRATION NUMBER: 1101-202
REFERENCE/DOCKET NUMBER: 1101-202
TELEEPHONIS: (212) 790-9090
TELEEPHONIS: (212) 790-9090
TELEERA: 6644 PENNIS
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LEMOTH: 12 aming acide
LEMOTH: 12 aming acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 3;
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66...
Grand Grandervative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: peptide US-08-602-999A-252
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KPMPPRPPL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: DUILLIM, Lawrence A.
APPLICANT: DER, Chauning J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: 1SOLATING AND USING SAME
Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
                                                                            COUNTRY: USA
ZIF: 19426-0107
COMPUTER: 19426-0107
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 252, Application US/08602999A Patent No. 6184205
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KAY, Brian K.
THORN, Judith M.
QUILLIAM, Lawrence A.
DER, Channing J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Savitzky, Marrin
REGISTRATION NUMBER: 29,699
REPERRNCE/DOCKET NUMBER: A135:
TELECOMMUNICATION INFORMATION:
TELERHONE: 610-454-3816
TELEFAX: 610-454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INPORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS: LENGTH: 11 amino acide TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                        Collegeville
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SPARKS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711
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GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTIVE TRRGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
FILE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/09/315,926A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 9201593.3
PRIOR APPLICATION NUMBER: EP 98201693.3
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                                                                                          NAME/KEY: SITE
1. LOCATION: (3)..(4)
1. LOCATION: (1)..(4)
1. LOCATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IOCATION: (5)...(6); OTHER INFORMATION: The Proline at these positions is a hydroxyproline. US-09-547-693-165
                                                                                                                                                                                                                                                           Gaps
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OTHER INFORMATION: Synthetic
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                            NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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82;
                                                                                                                                                                                                       43.5%; Score 30; DB 4; Length 8; 100.0%; Pred. No. 4.1e+05; attive 0; Mismatches 0; Indels
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; Sequence 18, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Bs van, Helmuth
; APPLICANT: Havenga, Menzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 165, Application US/09547693 Patent No. 6639050
    OTHER INFORMATION: Synthetic
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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Patent No. 6639050

GENERAL INFORMATION:
APPLICANT: Kallszewski, Marcia
APPLICANT: Kallszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 168
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09232446B
Patent No. 6228647
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Voytas, Daniel F.
APPLICANT: Gai, Xiaowu
TITLE OF INVENTION: Transposable Element Protein that Directs DNA
TITLE OF INVENTION: Integration to Specific Chromosomal Sites
FILE REFERENCE: 2-98
CURRENT FALING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1998-01-15
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66.7%; Pred. No. 4...
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                             , MOLECULE TYPE: peptide US-09-500-124-252
                                                                                                                                                                                                                                                                                                                                                 2 KAMDPTPPL 10
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                                                                                                                                         TYPE: amino acid
TOPOLOGY: unknown
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1 LDPSPP 6
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US-09-232-446B-24
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LENGTH: 6
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; OTHER INFORMATION: Description of Unknown Virus Organism: Artificial US-09-739-852-7
                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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US-08-271-698-2
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                                                                                                                                                    ; NAME/KEX: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage display peptide
US-09-315-926A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hayward, Diane S.
APPLICANT: Ling, Paul D.
TITLE OF INVENTION: EBNA2 PEPTIDES AND METHODS OF USING SAME
FILE REFERENCE: 97512
CURRENT APPLICATION NUMBER: US/09/133,341A
CURRENT PILING DATE: 1998-08-13
EARLIER PILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 3; Length 10;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                              42.0%; Score 29, DB 4; Length 12;
80.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-739-852-7; Sequence 7, Application US/09739852; Patent No. 6495144; GENERAL INFORMATION:
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 PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 12
                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                     4; Conservative
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Best Local Similarity
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Matches 4; Conserv
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ORGANISM: Unknown
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US-09-133-341-7
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LENGTH: 10
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Patent No. 5358934

GENERAL INFORMATION:

APPLICANT: Garlson, David A.

TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Pests

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1
Score 28; DB 4; Length 10;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 1; Length 6; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08271698; Patent No. 5439821; GENERAL INFORMATION: APPLICANT: BOTOVSKY, DOV; APPLICANT: Carlson, David A. TITLE OF INVENTION: Materials and Methods for Control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
PILING DATE: 19921211
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.1%;
  40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
TOPOLOGY: linear
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Search completed: May 26, 2005, 20:19:10 Job time : 41 secs
                                                                                                                                                                                                                                                          TELEPAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 39.1
Best Local Similarity 80.0
Matches 4; Conservative
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US-08-468-596-2
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Sequence 2, Application US/08468596;
GENERAL INFORMATION:
APPLICANT: Borcovsky, Dov
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Peats
NUMBER OF INVENTION: of Peats
STRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6;
                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: SAILWANCHIK, DAVIG R.

REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:

TELEFRENCE/DOCKET NUMBER: UF/S&S-127
TELEFRONE: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/468,596 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 1; Pred. No. 4.1e+05;
TITLE OF INVENTION: of Peats
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STREE: FL
COUNTR: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.1%; Score 27; DB Best Local Similarity 80.0%; Pred. No. 4.1e Matches 4; Conservative 0; Mismatches
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 DPTPP 9
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ANTI-SENSE: NO US-08-271-698-2
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Gaps
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80.0%; Pred. No. 4.1e+05;
tive 0; Mismatches 1;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,698
APPLICATION NUMBER: US/07/989,290
FILING DATE: 07-UUL-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGESTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8000
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 20:27:26; Search time 38 Seconds (without alignments) 20.256 Million cell updates/sec

US-10-047-945-7

1 LKAMDPTP 8 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

909 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 8 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Ω	major protein anti		alcohol dehydrogen	lectin - potato (f	ene	transferrin - bovi	T-cell receptor be	ICL2 protein - Par	enamelin f - bovin	leucokinin VII - M	Ca2+-transporting	tyrosine protein k	starvation-induced	ribosomal protein	proctolin - Americ	bis	proctolin - Atlant	halo-toxin - Pseud	DHLH transcription	244K exoantigen -	carboxylesterase (globulin IV alpha	adipokinetic hormo	neuropeptide Led-C	adipokinetic hormo	adipokinetic hormo	adipokinetic hormo	hypertrehalosemic
SUMMARIES	ΩI	B60274	151049	871919	S21288	PQ0008	A19780	PT0709	S71299	S10783	JS0317	I64832	I78890	S53508	S17255	HOROHA	PS0324	A60411	A61049	151317	A33098	809027	148086	990608	A33995	B44960	A58620	855310	810596	S08996
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	Query Match	6.5	41.9	1.9	9.5	2.5	30.2	30.2	30.2	.2	.2	.2	27.9	6.	27.9	6.7	6.7	27.9	6.7	6.7	6.7	6.7	7.9	27.9	7.9		7.9		7.9	7.9
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	Score	20	18	18	17	13	13	13	13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
	Result No.	1	7	E)	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

adipokinetic hormo endoglycosylcerami	hypothetical prote T-cell receptor be	cellulase (EC 3.2. leucopyrokinin - M	angiotensin-conver	sperm-activating p granulocyte-colony	D-mannonate hydrol cholecystokinin-5	20K protein – Rick Fc epsilon RIIb –	orf 3 rara 5'-regi mcrB protein - Esc
B49823 B39745	S16324 PT0530	S21273 A23967	A31570 E60588	G60588 I54017	157745 A32516	B31836 A46474	S15596 S55548
9 0	0 0	0 0	~ ~	0.4	0 0	0 0	40
27.9 8	27.9 8 27.9 8	27.9 8 27.9 8	27.9 8	27.9 8	25.6 4	25.6	25.6 6 25.6 7
12	12	122	12	12	##	11	11
30	33	34 35	36	8 8	40 41	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44 45

ALIGNMENTS

major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
B;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Title: Immun. 59, 372-382, 1991
A;Ritle: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: B60274
A;Accession: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG> ö Gaps ö Query Match 46.5%; Score 20; DB 2; Length 5; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 1; Indels 5 DPTP 8 RESULT 1 a ઠે

1 DPAP 4

metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Accession: 151049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) me A;Reference number: 151049
A;Accession: 151049
A;Accession: 151049
A;Accession: I51049
A;Accession:

ö Query Match 41.9%; Score 18; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels

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Gaps

4 MDP 6 გ.₋ გ

RESULT 3 871919 alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)

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monoferric fragments of bovine ti
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J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A.F. Feerence number: PT0509; MUID:91277601; PMID:1711558
A.Accession: PT0709
A.Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                transferrin - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993

C;Accession: A19780

R;Brock, J.H.; Esparza, I.; Oliver, R.A.; Spooner, R.L.

Biochem. Genet. 18, 851-860, 1980

A;Title: Electrophoretic mobility of N- and C-terminal monoferric fragments

A;Reference number: A19780; MUID:81183891; PMID:7225082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Paramecium terraurelia
Cibate: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
Cibacession: $71298
Cibacession: $71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0709
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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A,Restiques: 1-6 < PEB.
A,Experimental source: newborn thymus, strain BALB/c
C,Keywords: T-cell receptor
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Pred. No. 2.8e+05;
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Best Local Similarity
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1 AVNP 4
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                  3 AMDP
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    C;Species: Solanum tubercoum (potato)
C;Species: Solanum tubercoum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
F;Accession: S.2188 #13-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tubercosum L.) tuber. Characterizatio
A;Reference number: S21288 #WID:92272683; PMID:1590771
A;Molecule: 1P8 cMID: 92272683; PMID:1590771
A;Molecule: 1P8 cMID: A;Molecule: Nortein
A;Experimental source: var. Ulster Sceptre
C;Function: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin
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NyAlternate names: ficus latex peptide 1
('Species ratio carica (common fig)
C'Species: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C'Accession: PQ0008
R'Maruyama, S: Miyoshi, S: Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A,Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica. A,Recession: PQ0008
A,Recession: PQ0008
A,Molecule type: protein
A,Recession: PQ0008
A,Recessi
|Species: Ctenopharyngodon idella (grass carp)
|Pate: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
|Accession: S71919
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Best Local Similarity
Matches 3; Conserva
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2 ASTPSP 7
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2 DPT 4
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tyrosine protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: 178890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C. A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein A;Reference number: 158407; MUID:95060800; PMID:77970703
A;Recession: 178890
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
Plant Wol. Biol. 27, 477-485, 1995
A;Title: cDNA structure and regulatory properties of a family of starvation-induced ribo
A;Reference number: $53506; MUID:95201242; PMID:7894013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
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C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
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A;Variety: strain 07173
C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S17255
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                                                                                                                                              Length 8;
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Pred. No. 2.8e+05;
                                                                                                                                       Query Match 30.2%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 2; Conservative 0; Mismatches
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A;Molecule type: protein
A;Residues: 1-4 <KOE>
C;Genetics:
A;Gene: SERCAlb
C;Keywords: hydrolase
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C,Species: Rattus norvegicus (Norway rat)
R,Mu, K.
Am. J. Physiol. 264, 333-341, 1993
A,Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase in A,Reference number: I51892
A,Reference number: I51892
A,Reference number: I51892
A,Reference number: I51892
A,Reference number: I51893
A,Residues: 16832
A,Residues: 18 <-RES
A,Residues: 18 <-RES
A,Residues: 19 <-RES
A,Cross-references: UNIPROT:Q63139, GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646
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Cispecies: Leucophaea maderae (Madeira cockroach)
Cispecies: Solaii
Comp. Biochem. Physiol. C 88, 31-34, 1987
Comp. Biochem. Physiol. C 88, 31-34, 1987
A.Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the firm A.Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the firm A.Title: Leucokinins VII and VIII: the firm A.Molecule type: protein
A.Molecule
                                                                                                                                                                                                                                          RESULT 9
$10783
enamelin f - bovine (fragment)
c;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S10783
R;Strawich, E.; Glimcher, M.J.
Eur. J. Blochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
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Pred. No. 2.8e+05;
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   0; Mismatches
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A.Molecule type: protein
A.Residues: 1-8 <5TX>
C.Keywords: enamel; phosphoprotein
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Best Local Similarity 66.7
Matches 2; Conservative
2; Conservative
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                                                                     PTP 8
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A, Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from A, Reference number: $17255, MUD: 91285106; PMID: 2060626
A, A, Accession: $17255
A, ROJECULE type: protein
A, Residues: 1-4 < CRO>
A, CROSS-references: UNIPROT: P36515
C, Comment: A coding region for this protein could not be identified in the genome of Sac C, Genetics: A, Genome: nuclear
C, Reywords: mitochondrion; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Mocretie type: protein
A; Residues: 1-5 <STA>
A; Residues: 1-5 <STA>
A; Crose-references: UNIPROT: P01373
A; Octos-references: UNIPROT: P01373
A; Octos-references: UNIPROT: P01373
A; Octos: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac R; O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A; Title: Pentapeptide (proctolin) associated with an identified neuron.
A; Reference number: A94260; MUID: 8122865; PMID: 6113690
A; Contents: annotation; biological source
C; Comment: This peptide is found in the lateral white neurons, which occur (in the cockr innervate the striated hindgut muscles in insects and stimulate contraction of these mus C; Superfamily: proctolin
C; Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Periplaneta americana (American cockroach)
C.Species: Periplaneta americana (American cockroach)
C.Species: 29-JNL-1981 #sequence_revision 29-JNL-1981 #text_change 09-JNL-2004
C.Accession: A.N.; Brown, B.E.
Inife Sci. 17, 1253-1256, 1975
A.Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects A.Reference number: A93048; MUID:76074708; PMID:576
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C;Species: Periplaneta americar
C;Date: 29-1111-101 4--
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Gaps

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Query Match 27.9%; Score 12; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

6 PT 7

4 PT 5

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Search completed: May 26, 2005, 20:37:01 Job time: 44 secs

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"Protectly, ...... and A.A., rong W.P.; ploted delbus) liver alcohol dehydrogenase.";
Blochim. Biophys. Acta 1296:41-46(1996):
P.R.; 871919; 871919.
GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
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Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=235443;
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"Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding."; Biochem. J. 28:1818; 821288; S12188.

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                                  Length 8;
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STRAIN=H99;

STRAIN=H99;

Stuart L.T., Allen A., Dietrich F.S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY376718; AA088127.1; -.

GO; GO: 0004506; F: squalene monooxygenase activity; IEA.

MONOOXygenase; Oxidoreductase.

NON TER

SEQUENCE 8 AA, 811 MW; 0467776AABIDD727 CRC64;
                        DB 2; Leus
7. 1.6e+06;
0;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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924 MW; DEA9D411B1B76AB5 CRC64;
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                               Query Match 41.9%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 3; Conservative 0; Mismatches
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Solanum tuberosum (Potato)
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                                                                                                                                                Bacteriophage RB69.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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Kolesinskiene G., Nivinskas R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ458400; CAD30256.1; -.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ439452; CAD28423.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
03-03-2 protein (Fragment).
                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
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Similarity 75.0%;
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collision.

-!- SUBCELLULAR LOCATION: Secreted.
-!- DEVELOWINTLA. STAGE: First appears in the ovarian follicles furing vitellogenesis. Accumulates in the oocytes before being secreted during fertilization. Expression continues in the embedded oocyte. Accumulates in the egg capsule after fertilization.
-!- MASS SPECTROMETRY: MM=596.6; METHOD=MALDI; RANGE=1-6; NOTE=RRE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
"Isolation, identification and synthesis of locustamyotropin II, an additional neuropeptide of Locusta migratoria. Member of the cephalomyotropic peptide family.";
Insect Biochem. 20:479-484(1990).
-I- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                        TISSUE=Egg;
MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
Zatylny C., Marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide.";
Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-1- FUNCTION: Attracts sperm increasing the chances of gamete
        29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Sperm attracting peptide SepSAP.
Sepia officinalis (Common cuttlefish).
Bukaryota; Metazoa; Molluca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
                                                                                                                                                                     SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
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01-406-1991 (Rel. 19, Last sequence update)
05-401-2004 (Rel. 44, Last sequence update)
10-custamyotropin 2 (LOM-MT-2).
10-custamyotropin 2 (LOM-MT-2).
10-custa migratoria (Migratory locust).
10-custa migratoria (Migratory locust).
10-custa migratoria (Migratory locust).
10-custa migratoria (Migratory locust).
10-custa (Migratory locust).
10-custa (Migratory locusta).
10-custa (Migratory locusta)
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PROSITE; PS00539; PYROKININ; 1.
Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.6%; Score 14; DB 1; Length 6; Best Local Similarity 66.7%; Pred. No. 1.6e+06; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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6 AA; 597 MW; 72C8676AA0470000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA; 934 MW; 26341771A9CAA87B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity).
-!- SIMILARITY: Belongs to the pyrokinin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 14; DB 1; 1
75.0%; Pred. No. 1.6e+06;
ative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amidation; Direct protein sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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2 IDP
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SEQUENCE
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LMT2 LOCMI
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0
                        Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                  TISSUE-Epidermis;
MEDLINE-97165493; PubMed-9013254;
Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
Indentification and mRNA developmental profiles of two ultraspiracle isoforms in the epidermis and wings of Manduca sexta.";
Insect Mol. Biol. 6:41-53(1997).
EMBL; US7921; ARB64235.1;
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miaw S.C., Kang B.Y., White I.A., Ho I.C.; "A repressor of GATA-mediated negative feedback mechanism of T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miaw S.-C., Ho I.-C.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MsUSP-2 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Repressor of GATA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                   8 AA; 892 MW; F165BB0415A76B16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA; 943 MW; FE3411B771B6C766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 2; I
Pred. No. 1.6e+06;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF335542; AAG59843.1;
NON TER 8
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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PubMed=14688323;
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1 MEPS 4
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01-JUN-2001 (
01-JUN-2001 (
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ID SAPP_SEPOF
AC P83569;
DT 29-MAR-2004
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RESULT 8

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Q7 IMR4;
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                                                                                                                                                                                                                                                                                      americana.";
Regul. Pept. 71:199-205(1997).
-1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93197130; PubMed=8451173;
Nair J., Rouse D.A., Morris S.L.;
Nair J., Rouse D.A., Morris S.L.;
Nuclectide sequence analysis of the ribosomal S12 gene of
Mycobacterium intracellulare.";
Nucleic Acids Res. 21:1039-1039(1993).
-!- FUNCTION: One of the primary rRNA binding proteins, it binds
directly to 165 rRNA where it nucleates assembly of the head
domain of the 305 subunit. Is located at the subunit interface
close to the decoding center, probably blocks exit of the E-site
tRNA (By similarity).
-!- SUBUNIT: Part of the 305 ribosomal subunit. Contacts proteins S9
and S11 (By similarity).
-!- SIMILARITY: Belongs to the ribosomal protein S7P family.
                                                                                                                                                                                                            SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
TISSUB=Corpora cardiaca;
MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLUTAR LOCATION: Secreted.
-1- MASS SPECTROMETRY: MW=907.92; METHOD=Electrospray; RANGE=1-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kinin-3 (Pea-K-3).
Periplaneta americana (American cockroach).
Bukaryyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteracioda; Dictyoptera; Blattaria; Blattoidea; NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium intracellulare.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0: Indels
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Pred. No. 1.6e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           NOTE=Ref.1.

-1- SIMILARITY: Belongs to the kinin family.
Amidation; Direct protein sequencing; Neuropeptide.
MOD_RES 8 Glycine amide.
SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
30S ribosomal protein S7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%;
Similarity 66.7%;
2; Conservative
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                                                             STANDARD;
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                            activity)
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P33564;
                                                             PK3 PERAM
P82687;
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RS7_MYCIT
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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TISSUB=Bone marrow;
MEDLINE=95002916; PubMed=7919324;
Tighe J.E., Calabi F.;
Tighe J.E., Calabi F.;
Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                      EMBL; L08171; AAA25376.1; -.
PIR; S35538; S35538.
HAWAP; MP_00480; -; 1.
InterPro; IPR000235; Ribosomal_S7.
PROSITE; PS0052; RIBOSOMAL_S7; PARTIAL.
Ribosomal protein; RNA-binding; rRNA-binding.
INIT MET 0 BY similarity.
NON_TER 8
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATF synthase beta subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood 84:2115-2121(1994).
BmBL; 874094; AAD14973.2; -.
NON TER
SEQÜENCE 8 AA; 929 MW; 30B764405B17244B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;
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Pred. No. 1.6e+06;
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Name=runt/68nt/MTG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.6%;
50.0%;
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Brassica napus (Rape).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:621-628(2000).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryozy, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Leptospermum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%; Score 14; DB 2; Length 8; 50.0%; Pred. No. 1.6e+06; ative 2; Mismatches 0; Indels
                                                                                                                                                                                                    Zhang Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF264734; AAF74768.1; -.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Heslewood M., Quinn C.J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184690; AAF03860.1; -.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9TKES;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                Chloroplast.

NON TER 8 8
SEQUENCE 8 AA; 919 MW; ECAIBIB764404406 CRC64;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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                                                                                                                                                                      SEQUENCE FROM N.A.
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3 INPT 6
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NON TER
SEQUENCE 8 A
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097KES
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AC 097KES
DT 01-MA;
DT 01-JM,
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Search completed: May 26, 2005, 20:36:15 Job time : 176 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 20:18:30; Search time 157 Seconds (without alignments) 19.708 Million cell updates/sec

US-10-047-945-7 1 LKAMDPTP 8 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

160390 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 8 Minimum DB Maximum DB M Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database

geneseqp2003as:*geneseqp2003bs:* geneseqp2001s:*geneseqp2002s:* geneseqp2000s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Abb80228 Synthetic	Aaw53842 N-terminu	Abb80224 Synthetic	Aaw45995 Peptide #	Adk10228 Human pap	Aar37031 Pentapept	Aab68473 Mutated p	Aay50089 Coxsackie	Abr82052 N-termina	Adk01475 Hepatitis	Aab74035 Partial s	Abb81338 Human VPL	Aaw24922 Vesicular	Aab74036 Synthetic	Abb81339 Human VPL	Aay40821 Amino aci	Aab17247 SH3 antag	Aab17233 SH3 antag	Aab17232 SH3 antag	Aab30156 Scaffold	Aam46490 H11 bindi	Aam46495 H11 bindi	Aam45098 H11 bindi	Aam44790 H11 bindi	Abb73240 Src homol
ΩI	ABB80228	AAW53842	ABB80224	AAW45995	ADK10228	AAR37031	AAB68473	AAY50089	ABR82052	ADK01475	AAB74035	ABB81338	AAW24922	AAB74036	ABB81339	AAY40821	AAB17247	AAB17233	AAB17232	AAB30156	AAM46490	AAM46495	AAM45098	AAM44790	ABB73240
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& Query Match	100.0	55.8	55.8	55.8	55.8	53.5	53.5	53.5	51.2	51.2	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8
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Abb73226 Src home Abb73225 Src home Adc44630 Endothel Adj73394 SH3 ante Adj73310 SH3 ante Adj73313 CH1 dele Adj53012 CH1 dele Adj53028 CH1 dele Adj51974 CH1 dele Adj51989 CH1 dele Adj51989 CH1 dele Adj51989 CH1 dele Adj51989 CH1 dele Adj51989 CH1 dele Adj51989 CH1 dele Adj61989 CH1 dele	Adg2853 196 Adq07145 196 Adq07268 196 Abp12619 HIV Abp20550 HIV
7 5 ABB73226 7 7 ADC44630 7 7 ADC47630 7 7 ADJ73394 7 7 ADJ73380 7 8 ADJ53013 7 8 ADJ53014 7 8 ADJ51974 7 8 ADJ51989 7 8 ADJ61989 7 8 ADG61989	
26 27 29 29 30 30 31 31 31 32 32 33 32 33 33 34 34 35 37 37 37 37 37 37 37 37 37 37 37 37 37	21111211

## ALIGNMENTS

ABB80228 standard, peptide, 8 AA.

ABB80228;

(first entry) 06-NOV-2003

Synthetic LINF, LT-8.

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA. 

Synthetic.

WO2003060471-A2.

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

e.g. Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deamlinase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (BLISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                      Length 8;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                    100.0%; Score 43; DB 7; Le
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW53842 standard; peptide; 5 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   histamine reaction treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminus of opossum LTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                      LKAMDPTP
                                                                                                                                                                                                                                                                                                                                1 LKAMDPTP
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                                                                                                                                                                                                                 Sequence 8 AA;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IGB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGB levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid athritis, Sjogren's syndrome, Relier's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas lood requires colting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                              Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                 ;
0
                                                                                 Indels
                                                Length 5;
                                              DB 2; Le
. 1.8e+06;
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                                                                                 Mismatches
                                              Score 24;
Pred. No.
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                                                55.5%,
100.0%; Pre-
                                                                                                                                                                                                                                          ABB80224 standard; peptide; 5 AA.
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                                              55.8%;
                                                                                                                                                                                                                                                                                                               06-NOV-2003 (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                 Synthetic LINF, LT-5.
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                                                             Local Similarity
nes 5; Conserv
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              Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                              Query Match
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                                                                                 Matches
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Matches

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AAW45995

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reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a novel polypeptide encoded by an alternative
                                         pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 8; Length 8; Pred. No. 1.8e+06; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              component #1 of N-linked glycoconjugate.
       Human papillomavirus peptide #2283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 198; 220pp; English.
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                                                                                                                                                                                                                                                                                                                      Habel
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                                                                                                                                                                                                                               24-JUL-2002; 2002AT-00001124.
11-JUL-2003; 2003EP-00450171.
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                                                                                                                                                                                                                                                                                                                      Schmidt W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                           Human papillomavirus
                                                                                                                                                                                                                                                                                   (INTE-) INTERCELL AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1991;
11-AUG-1992;
                                                                                                                                                              05-FEB-2004.
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28-JUL-1993
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                                                                                                                                                                                                                                                                                                                      Mattner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR37031;
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Matches
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AAR37031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New non-naturally occurring peptide(s) - which are based on portions of somatostatin, somatostatin receptors and insulin-like growth factor binding protein.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                    Hormone, receptor, antibody, vaccine, immunogen, somatostatin, IGF; insulin-like growth factor binding protein; ILGFBP, SSTR; diabetes; somatostatin receptor; insulin-like growth factor.
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   55.8%; Score 24; DB 7; Length 5; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.8%; Score 24; DB 2; Length 8; 66.7%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                    Peptide #17 based on human SSTR 2 (residues 282-290).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kingston DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3xample 10; Page 9; 136pp; English
                                                                                                                                                                                             AAW45995 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                 (first entry)
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                                     5; Conservative
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Query Match
Best Local Similarity
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                                                                        1 LKAMD 5
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AISPTP (
                                                                                                        LKAMD
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9744352-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1996;
                                                                                                                                                                                                                                                                 03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerraty NL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                               AAW45995;
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AC ADK1
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us-10-047-945-7.closed.rag

Dwek RA,

(MONS ) (OXFO-)

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specification describes a method for targeting integration of refrences a method for targeting integration of refrontial second integration of Tyl-copia group to desired location on a chromosome. The method uses a modified integrase in a retrotransposon, where the modified integrase contains a coding sequence for a peptide portion which specifically binds to protein bound to the chromosome or to particular nucleic acid sequences on chromosome. The method is useful for targeting integration of a retrotransposon of the Tyl-copia group to a desired chromatin targeting of Tys is useful for targeting chromatin targeting of Tys is useful for tagging genes which are affected by aging and for studying oncogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a conserved Coxsackievirus A (serotype A16) VP1 epitope. The invention relates to a novel method for designing degenerate PCR primers (AAZ30975-Z31000, AAZ3261- AAZ3261) for amplifying target polynucleotides. This method comprises identifying uniquely conserved amino acid sequences (e.g, this epitope) in target proteins, synthesising degenerate polynucleotides encoding the conserved sequences; and substituting the synthesised polynucleotides with up to four predetermined nucleotides (e.g., inosine) at degenerate nucleotide positions. The nucleic acids comprise no more than 7 degenerate positions, have no more than 2 adjacent predetermined nucleotides and the
present sequence represents a mutated portion of an integrase. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virus; epitope; target; degenerate; PCR; primer; amplification; VP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural protein 2A, conserved, base analogue, inosine, predetermined nucleotide, diagnosis, enterovirus; poliovirus
                                                                                                                                                                                                                                                                                                                         Score 23; DB 4; Length 6;
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Designing degenerate polymerase chain reaction primers.
                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coxsackievirus A VP1 conserved epitope 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 18; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY50089 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                    53.5%;
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                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
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N-PSDB; AAZ32608.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                4 MDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -|-:
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                                                                                                                                                                                                                                                                              Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                         AAR37031-3 or an atriopeptin e.g. atriopeptin A or D, see AAR37337-8) having an activated carboxyl group capable of forming a betaglycosylamine linked glycoconjugate is reacted with an unprotected betaglycosylamine deriv. of an oligosaccharide. The deriv. is prepared by reacting an unprotected oligosaccharide having up to 9 saccharide units with saturated ammonium bicarbonate at pH 8.0-8.5. The N-linked glycoconjugate is produced under conditions to directly maintain the beta-anomeric configuration. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Targeting integration of retrotransposon or retrovirus into silent chromatin by transforming a cell with modified integrase having a coding sequence for a peptide portion that interacts with chromatin at desired
                                                                                                                                                                               N-linked peptide glyco-conjugate(s) prepn. - by reacting oligosaccharide(s) with ammonium bi:carbonate to maintain beta-anomeric configuration, and avoid sepn. of anomers.
                                                                                                                                                                                                                                                                                                                         peptide of 5-25 amino acid residues (pref. one of the pentapeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin; chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
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1.8e+06;
                                                                                            Wong SYC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.5%; Score 23; DB 100.0%; Pred. No. 1.8 ive 0; Mismatches
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                                                                                          Manger ID, Rademacher TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB68473 standard; peptide; 6 AA.
                                             OXFORD GLYCOSYSTEMS LTD.
                                                                                                                                                                                                                                                                            Claim 3; Page 32; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Col 66; 41pp; English.
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                          MONSANTO CO
                                                                                                                                    WPI; 1993-128045/16
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Best Local Similarity
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15-JAN-1999; 15-JAN-1998;

US6228647-B1

08-MAY-2001

23-JUL-2001

AAB68473;

RESULT 7 AAB68473

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Sequence 5 AA;

Matches

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predetermined nucleotides are 3 bases away from the 3' end of the synthesised strand. The degenerate primers are useful for amplifying target polynucleotides by the polywarease chain reaction (PCR). The use of the method of designing degenerate primers useful for the detection of polioviruses in clinical samples is described in USSSS477. The degenerate primers facilitate PCR amplification of unknown polynucleotides, where the amino acid sequence encoded is known. The primers also allow for the subsequent molecular based diagnosis with a serologically derived diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method of screening for a compound that modulates the binding of an oligosaccharide to a beta subunit of AMP kinase. The method comprises: (1) exposing a candidate compound to an oligosaccharide and a polypeptide comprising a beta subunit of AMP kinase, or its mutant and/or fragment that binds an oligosaccharide; and of the polypeptide to the candidate compound to modulate binding of the polypeptide to the oligosaccharide. An AMP kinase beta subunit oligosaccharide binding domain sequence has antidiabbetic, cycostatic, antiarteriosclerctic and anorectic activities, and can be used in gene therapy. The method is useful for screening for a compound that modulates the binding of an oligosaccharide to a beta subunit of AMP kinase for treating or preventing a condition associated with AMP kinase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for a compound that modulates the binding of an oligosaccharide to a beta subunit of AMP kinase by assessing the ability of the candidate compound to modulate binding of the polypeptide to the oligosaccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g., diabetes, atherosclerosis, obesity or cancer. The present sequence represents an N-terminal sequence from AMPK beta 1 (68-163) fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMP kinase beta subunit oligosaccharide binding domain; AMP kinase; oligosaccharide binding domain; enzyme; antidiabetic; gene therapy; antiarteriosclerotic; anorectic; cytostatic; diabetes; atherosclerosis; obesity; cancer; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal sequence from AMPK beta 1 (68-163) fusion protein SEQ ID:31.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                  3; Indels
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Pred. No. 1.8e+06;
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57.1%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-2001; 2001AU-00009728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton D, Kemp BE;
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                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                           2 KAMDPTP
                                                                                                                                                                                                                                                                                                                                                              KXTDPPP
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                                                                                                                                                                                                      Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR82052;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a hepatitis C virus peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel polypeptide encoded by an alternative
                                                                                             Gaps
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protein, which is used in an example from the present invention
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                                                                                             0; Indels
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Pred. No. 1.8e+06;
3; Mismatches 2; Indels
                                                            51.2%; Score 22; DB 6; L 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus 1b peptide SeqID127.
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                                                                                                                                                                                                                                     ADK01475 standard; peptide; 8 AA.
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11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                                                                 06-MAY-2004 (first entry)
                                                                           Local Similarity 100.
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Best Local Similarity 37.5
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattner F, Schmidt W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INTE-) INTERCELL AG.
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                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus
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                               Sequence 7 AA;
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                                                            Query Match
Best Local S
Matches 4
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ID AAB7
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AAB74035;

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The present invention describes an antibody which specifically recognises the human VPLF (vascular endothelial growth factor (VEGF)/plateletactive derived growth factor (PEGF)/plateletactive of this protein as growth factor. The antibody has vasotropic, vulnerary, nephrotropic, cardiant, antidiabetic, antiarteriosclerotic, antianaemic, osteopathic, anticheumatic, antiarthritic and antipsoriatic activities. The antibody is applicable in diagnostics and remedies for VPLF-participated diseases like arthritis, ischaemic diseases and retarded wound healing. The present sequence represents a human VPLF related peptide sequence, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Etiological agent; autoimmune disease; systemic lupus erythematosus; SLE; Ro/SSA; immunoreactive; autoantibody; antigenicity; nucleocapsid;
                                                                                                                                                                                                                        Antibody specifically recognizing VPLF or its variant and inhibiting its activity, applicable in diagnostics and remedies for VPLF-participating diseases like arthritis, ischemic diseases and retarded wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of immunogenic agent in auto-immune disease - by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 5; I
Pred. No. 1.8e+06;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                          Example, Page 59; 136pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24922 standard; peptide; 5 AA.
19-OCT-2001; 2001WO-JP009218.
                                                                              (KYOW ) KYOWA HAKKO KOGYO KK. (HELI-) HELIX RES INST.
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                                        19-OCT-2000; 2000JP-00319985.
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                                                                                                                                           Furuya A;
                                                                                                                                                                                    WPI; 2002-394558/42.
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es 3; Conserv
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31-JAN-1991;
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17-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence sequence is provided in a specification relating to a novel vascular endothelial growth factor (VEGF)/platelet derived growth factor (PEGF)-like factor of 345 amino acids, or to a sequence in which at least one amino acid is deleted, replaced or added compared to the native sequence. The nucleotide sequence encoding the VEGF/PDGF-like factor may be integrated into a vector and used to transform a host cell. The VEGF/PDGF-like factor may be used in the development of agents for transform and the treating diseases associated with abnormal neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; VPLF; VEGF/PDGF-like factor; vascular endothelial growth factor; platelet-derived growth factor; antibody; inhibition; growth factor; vasotropic; varietiabetic; antianaemic; antianaemic; antianaemic; antianaemic; antianaemic; antipsorietic; osteopathic; antirheumatic; antiantic; antipsoriatic; arthritis; ischaemic disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New VEGF/PDGF-like factor useful for the development of treating agents for diseases accompanied by accentuation of abnormal neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                   Partial sequence contained in commercially available plasmid pMbac.
                                                                                                                                         VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF; platelet derived growth factor; PDGF; neovascularisation; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human VPLF related peptide sequence SEQ ID NO:34.
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(HERI-) HERIKKUSU KENKYUSHO KK.
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                                                           (first entry)
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Best Local Similarity 75.0
Matches 3; Conservative
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DPSP 4
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                                                           09-AUG-2001
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ABB81338;

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Gaps

Sequence 6 AA;

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The invention relates to methods to determine the etiological agent of autoimmune diseases such as systemic lupus erythematosus (SLB). A common antigen for SLE and closely related disorders is the 60 kD protein-RNA particle: Ro/SSA, present in all calls studied to date. Staphylococcus VB protease digestion of this protein reveals bands of 51, 40, 35, 28 and 13 kD which are strongly immunoreactive with SLE autoantibodies. From the 13 kD band, peptide AAWA-911 demonstrated maximal antigenicity against anti-Ro/SSA autoantibodies beptides immunoreactive with SLE autoantibodies can then be used to screen for other peptides reactive with the antibodies. An example of such a peptide is the sequence presented here which is derived from the nucleocapsid protein of the Indiana serotype of the vesicular stomatitis virus. (Updated on 25-MAR-2003 to correct PP
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identifying protein sequences homologous to self-antigen sequences.
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                                                            Example 2; Col 17; 36pp; English.
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                                                                                                                                                                                                                                                                                                                    Human, VPLF; VBGF/PDGF-like factor; vascular endothelial growth factor; platelet-derived growth factor; antibody; inhibition; growth factor; assorropic; valnerary; nephrotropic; cardiant; antidiabetic; antianaemic; antiarteriosclerotic; octeopathic; antirheumatic; antiarthritic; antipsoriatic; arthritis; ischaemic disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody specifically recognizing VPLF or its variant and inhibiting its activity, applicable in diagnostics and remedies for VPLF-participating diseases like arthritis, ischemic diseases and retarded wound healing.
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                Score 21; DB 4; Length 6;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                    Human VPLF related peptide sequence SEQ ID NO:35.
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                                                                                                                                                                                           ABB81339 standard, peptide; 6 AA.
                48.8%;
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Query Match
Query Match
Best Local Similarity 75.00,
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nes 3; Conserv
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Search completed: May 26, 2005, 20:33:20 Job time : 164 secs

Sequence 26, App. Sequence 29, Appl Sequence 34, Appl Sequence 35, Appl Sequence 4, Appli

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Sequence 29, Ay Sequence 20, 3 Sequence 23, 3

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US-09-758-198-29
US-09-861-661-20
US-09-861-661-23
US-09-861-661-23
US-09-861-661-23
US-09-861-661-23
US-10-399-673-35
US-10-399-673-35
US-10-399-673-35
US-10-399-673-35
US-10-286-457-359
US-10-286-457-359
US-10-609-217-289
US-10-609-217-289
US-10-651-723-289
US-10-651-723-289
US-10-651-723-289
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RESULT 1
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| cgn2_6/ptodata1/foubpaa/US07_PUBCCMB.pep:*
| cgn2_6/ptodata1/foubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata1/foubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata1/foubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata1/foubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata1/foubpaa/US08_PUBCOMB.pep:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-758-128-23
US-09-758-128-29
US-09-758-128-29
US-09-758-426-20
US-09-758-426-29
US-09-758-426-29
US-09-758-198-20
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US-09-758-198-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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Match Length
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Maximum DB
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                                                    APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (198) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
LEWARTH: B
LEWARTH: B
LEWARTH: B
LEWARTH: B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 43; DB 14;
100.0%; Pred. No. 1.3e+06;
cive 0; Mismatches 0;
Sequence 7, Application US/10047945; Publication No. US20030157555A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
COTHER INFORMATION: Synthetic.
US-10-047-945-7
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.8; Conservative
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RESULT

23,

Sequence Sequence Sequence

Sequence

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APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE REFERENCE: 1045786/0214
CURRENT PAPLICATION NUMBER: US/09/758,128
CURRENT PLING DATE: 2001-01-12
PRIOR PILING DATE: 1990-02-05
PRIOR PILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PALENTIN VEr. 2.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09758128

Sequence 26, Application US/09758128

Patent No. US20020107187A1

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: GERRATY, No. US20020107187A1man L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: 09/194,218

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

NUMBER OF SEQ ID NOS: 58

SOFTWARRE: Patentin Ver. 2.0

SEQ ID NO 26
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Patent No. US20020107187A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187A1man L.
APPLICANT: WESTEROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
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Pred. No. 1.3e+06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 9;
Pred. No. 1.3e+06;
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Best Local Similarity
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Matches 4; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Porcine
US-09-758-128-23
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US-09-758-128-29
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Sequence 20, Application US/09758128

Batent No. US20020107187A1

GENERAL INVENTATION:

APPLICANT: KINGSTON, No. US20020107187A1man L.

APPLICANT: WESTBROOK, Simon L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/758,128

CURRENT APPLICATION NUMBER: 09/194,218

PRIOR FILING DATE: 1996-05-05

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 20

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         Sequence 3, Application US/10047945
Publication No. US20030157555A1
Sequence 1, INFORMATION:
APPLICANT: LIPPS, BREDERICK W.
APPLICANT: LIPPS, BREDERICK W.
APPLICANT: LIPPS, BREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E TITLE OF INVENTION: (198) IMPLICATED DISORDERS
FILE REPERENCE: FWLPAT015US
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE:
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SOFWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 3
LENGTH: 5
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; Sequence 23, Application US/09758128
; Patent No. US20020107187A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: SYNTHESIZED. OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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US-09-758-128-20
US-10-047-945-3
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TYPE: PRT
ORGANISM: Mouse
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Fatent No. US20020169116A1

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: WISTERROW, Simon L.

APPLICANT: WISTERROW, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: PEPTILES, ANTIBODIES, VACCINES AND USES THEREOF

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: 09/194,218

FRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATENTIN VOICE OF SEQ ID NOS: 58

LENGTH: B
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Patent No. US20020169116A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020169116A1man L.
APPLICANT: WESTRANOCK, Simon L.
APPLICANT: WESTRANOCK, Simon L.
APPLICANT: WINDERTON: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT FILING DATE: 2001-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PACENTIN VEr. 2.0
SEQ ID NO 29
LENGTH: 8
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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1 AISPTP 6
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; ORGANISM: Bovine
US-09-758-426-20
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; ORGANISM: Rat
US-09-758-128-29
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US-09-758-426-23
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GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: GENERATY, No. US20020169116Alman L.
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION UNMERR: US/09/758,426
CURRENT APPLICATION NUMBER: 09/194,218
FRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN USE: 2.00
SEQ ID NO 26
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Patent No. US20020169116A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: WESTERROX, Simon L.
APPLICANT: WESTERROX, Simon L.
TILLE OF INVENTION: WODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TILLE OF INVENTION: PEPTINES, ANTIBODIES, VACCINES AND USES THEREOF
CURRENT PELICATION NUMBER: 09/194,218
FRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR PELING DATE: 1999-02-05
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.3e+06;
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; Sequence 26, Application US/09758426
; Patent No. US20020169116A1
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN'
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver: 2.0
LEGORIH: 8
LENGTH: 8
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
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f ORGANISM: Porcine
US-09-758-426-23
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1 AISPTP
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US-09-758-198-29
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LENGTH: 8
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Publication No. US20020187925A1
GENERAL INFORMATION:
APPLICANT: GERRATY, No. US20020187925A1man L.
APPLICANT: WESTRROWE: Simon L.
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/758,198
CURRENT FILING DATE: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-02
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1996-05-22
PRIOR APPLICATION NUMBER: BARLIER PILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SCFWARRE: PACENTER PILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 20
LENGTH: 8
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Publication No. US20020187925A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GENERATY, No. US20020187925A1man L.
APPLICANT: GENERATY
NOULANING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PRETIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION: - PRETIDES, ANTIBODIES, VACCINES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/758,198
CURRENT FILING DATE: 2001-01-12
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SCOFFWARE: PATCHLIN VET. 2.0
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Pred. No. 1.3e+06;
1; Mismatches 1; Indels
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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1 AISPTP 6
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1 AISPTP 6
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ORGANISM: Bovine
                                                 ; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-29
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US-09-758-198-20
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US-09-758-198-23
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SEQ ID NO 29
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Sequence 26, Application US/09758198

Publication No. US20020187925A1

GENERAL INFORMATION:
APPLICANT: GERRATY, No. US20020187925A1man L.
APPLICANT: MESTERRONE: 106786/0214

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REPREBENCE: 106786/0214

CURRENT APPLICATION NUMBER: US/09/758,198

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: BARLIER FILING DATE: 1999-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-22

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990

PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

NUMBER OF SEQ ID NOS: 20

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Sequence 29, Application US/0020187925A1

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: KINGSTON, David J.

APPLICANT: MESTRATY, No. US20020187925A1man L.

TITLE OF INVENTION: PERTIDES, ANTIBODIES, VACCINES AND USES THEREOF

TITLE OF INVENTION: PERTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 29

LENGTH: 8
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                                                                                                                                                                 Score 24; DB 9; I
Pred. No. 1.3e+06;
1; Mismatches 1;
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Pred. No. 1.3e+06;
1; Mismatches 1;
                                                                                                                                                                 55.8%;
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SEQ ID NO 26
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Best Local Similarity 66.
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Best Local Similarity 66.7
Matches 4; Conservative
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; TYPE: PRT
; ORGANISM: Porcine
US-09-758-198-23
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US-09-758-198-26
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                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                              RESULT 15
US-09-861-661-20

i Sequence 20, Application US/09861661

i Publication No. US20030045676A1

i GENERAL INFORMATION:

APPLICANT: KINGSTON, DAVID J.

APPLICANT: WESTERSON, DAVID J.

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF

FILE REFERENCE: 04270/0135

CURRENT APPLICATION NUMBER: US/09/861,661

CURRENT PILING DATE: 2001-05-22

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-05-22

NUMBER: OF SEQ ID NOS: 59

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 20

LENGTH: BATCH OF SECOLED NOS: 20

SECOLED NO 20
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                                                                                                                  1; Indels
                                                                            55.8%; Score 24; DB 9; Length 8; 66.7%; Pred. No. 1.3e+06; ive 1; Mismatches 1; Indels
                                                                          Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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|: |||
1 AISPTP 6
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1 AISPTP 6
                                                                                                                                                        3 AMDPTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: BOB BD.
US-09-861-661-20
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-29
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Search completed: May 26, 2005, 20:49:24 Job time : 157 secs This Page Blank (uspto)

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Sequence 27, Sequence 64, Sequence 66,

Sequence : Sequence : Sequence Sequence 1, A Sequence 1, A Sequence 1, A Sequence 70, Sequence 46, Sequence 72, Sequence 70,

Sequence 72, Sequence 46, Sequence 70, Sequence 72,

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

Perfect score:

Sequence:

OM protein

Run on:

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US-69-67-163A-3

1 Sequence 3, Application US/08657163A

1 Patent No. 5744449

1 GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

TITLE OF INVENTION: SYNTHETIC LITRES AND THEIR

TITLE OF INVENTION: SYNTHETIC LITRES AND THEIR

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSES: BINIE V. LIPPS

STREET: TEXAS

COUNTRY: BELLAIRE
STREET: TEXAS

COUNTRY: USA

STREET: TEXAS

CONFUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

COMPUTER: SETION DATA:
APPLICATION NUMBER: US/08/657,163A

FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: 108/058,387

FILING DATE: 2 SEPTEMBER 1994

CLASSIFICATION NUMBER: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 20,198

REGISTRATION NUMBER: 28,198

REGISTRATION NUMBER: 28,198

REGISTRATION NUMBER: 28,198

REGISTRATION NUMBER: 28,198
US-08-473-489A-190
US-08-48-695-190
US-07-657-769B-25
US-07-657-769B-27
US-07-657-769B-64
US-07-657-769B-64
US-07-989-290-1
US-08-290-1
US-08-200-1
US-08-475-263-70
US-08-475-263-70
US-08-485-886-70
US-08-485-886-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMINO ACID
DEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N
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7, Appl

2, Appl

2, Appl

2, Appl

8, Appl

88, Appl

88, Appl

68, Appl
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                                                                                                                                     May 26, 2005, 20:30:57 ; Search time 40 Seconds (without alignments) 14.930 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-428-082B-289
US-09-428-082B-303
US-077-789-184-190
US-08-475-263-190
US-08-477-152-190
US-08-477-141-190
US-08-477-141-190
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US-07-926-786-1

US-07-926-786-1

US-09-147-933-35

US-08-66-473-60

US-07-657-769B-1

US-07-657-769B-2

US-07-657-769B-2

US-08-67-769B-2

US-08-135-198-20

US-08-135-198-20

US-08-475-263-68

US-08-477-362-68

US-08-477-362-68

US-08-485-68-68

US-08-485-68-08

US-08-485-68

US-08-485-68

US-09-295-316-4

US-09-428-082B-289

US-09-428-082B-289

US-09-428-082B-289

US-09-428-082B-289

US-09-428-082B-289

US-09-428-082B-309

US-09-488-68-68-309

US-09-48-082B-309

US-09-48-082B-309

US-09-48-082B-309

US-09-48-082B-309

US-09-48-082B-309

US-09-48-082B-309

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US-08-48-886-190

US-08-48-886-190
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                                                                                                                                                                                                                                                                                                                                                                  513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                1 LKAMDPTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 8
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1 KXTDPPP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LDPSP
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US-09-147-933-35
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                                                                                                                                                                                                                                                                                                               APPLICANT: Rademcher, Thomas W.
APPLICANT: Rademcher, Ian D.
APPLICANT: Wong, Simon
APPLICANT: Dwek, Raymond A.
TITLE OF INVENTION: Method for Producing Synthetic N-Linked
TITLE OF INVENTION: Glycoconjugates
NUMBER OF SEGUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.5%; Score 23; DB 1; Length 5; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                         0; Indels
                                                        Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRAINERS STATE TORM:

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/926,786

TITING DATE: 19920811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG STREET: 800 N. Lindbergh Blvd. CITY: St. Louis STATE: Missouri
                                                    55.8%; Score 24; DB 1; Ld 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA,
APPLICATION NUMBER: US 07/776911
FILING DATE: 15-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/394691
FILING DATE: 16-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-232-446B-24
; Sequence 24, Application US/09232446B
                                                                                                                                                                                                                          RESULT 2
US-07-926-786-1
'S Sequence 1, Application US/07926786
'Patent No. 5280113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyer, Scott J. S. 275
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (314)694-3117
TELEPAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
; ORIGINAL SOURCE: SYNTHETIC US-08-657-163A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.5
Best Local Similarity 100.
Matches 4; Conservative
                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 14m2-
                                                                                                                                 1 LKAMD 5
                                                                                                                                                                1 LKAMD 5
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GENERAL INFORMATION:

APPLICANT: VOYLES, Daniel F.

APPLICANT: Gai, Xiaowu

TITLE OF INVENTION: Transposable Element Protein that Directs DNA

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

CURRENT APPLICATION NUMBER: US/09/232,446B

CURRENT APPLICATION NUMBER: US 60/071,383

PRIOR APPLICATION NUMBER: US 60/071,383

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 24

LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: mxutant peptide ; OTHER INFORMATION: sequence US-09-232-446B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 35, Application US/09147933A

Patent No. 6168917

GENERAL INFORMATION:
APPLICANT: Kilpatrick, David
TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: NON-POLIO ENTEROVIRUSES
FILE REFRENCE: 62224/04

FILE REFRENCE: 62224/04

CURRENT APPLICATION NUMBER: US/09/147,933A

CURRENT FILING DATE: 1999-07-09

EARLIER APPLICATION NUMBER: U. S. 60/027,353

EARLIER FILING DATE: 1996-10-01

EARLIER FILING DATE: 1996-10-02

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FASSERE OF Windows Version 3.0

SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 3; I Pred, No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 3;
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches

    LOCATION: (2) ...(2)
    OTHER INFORMATION: "RESIDUE 2 = LEU OR MET"
    OTHER INFORMATION: peptide
    US-09-147-933-35

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.5%;
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                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
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Score 21; DB 1; Length 5; Pred. No. 4.1e+05; 1; Mismatches 1; Indels
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Patent No. 5256766
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: PHARMACEUTICALS
INTER OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
FLING DATE: 19910219
FLING DATE: 19910219
ATTORNEY/AGENT INFORMATION:
NAME: MURABIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0502:00
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPAM: 415-327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPTIFE 940.2

CARPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: MUTASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 29,959
REJERRENCE/DOCKET NUMBER: 2000-0502.00
TELEBOMMUNICATION INFORMATION:
TELEBOMMUNICATION INFORMATION:
TELEBOMMUNICATION 187-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.8%;
           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
STRANDEDNESS: Bingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MDPTP 8
             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LDPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CP
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-657-769B-1
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APPLICANT: YOSHIDA, ATUTO
APPLICANT: TAKEUCHI, MAKOTO
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCE: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Patent No. 5256766
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF INVENTION: PHARMACEUTICALS
NUMBER OF SHOUGHCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MEMIO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 7;
                                                                                                                                                                                                                                                                                            COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION NUMBER: WP PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION NUMBER: US/08/50238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION NUMBER: 10 - 269111
FILING DATE: 09-FEB-1995
PRIOR APPLICATION NUMBER: 29,768
ATYONEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
RESERENCE/DOCKET NUMBER: 16887/837
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEERAK: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBERING (202,
TELBERY 904136
INFORMATION FOR SEQ ID NO: 60
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TVPE: amino acids
TVPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66...
                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
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Gaps

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1 LKAMD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-335-198-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                         Gaps
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Patent No. 5637454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41
COMMESSPONDENCE ADDRESSES:
ADDRESSEER: 1100 Peachtree Street, Ste. 2800
                                                                                                                                                                                          KESULL A

US-07-657-769B-62

Sequence 62, Application US/07657769B

PATENT NOT SERVICE

TITLE OF INVENTION:

TITLE OF INVENTION: PHARMACEUTICALS

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: IRELL & MANELLA

STREET: 545 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK

STATE: CA

COUNTRY: USA
                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%; Score 21; DB 1; Length 5; 60.0%; Pred. No. 4.1e+05; ive 1; Mismatches 1; Indels
                   48.8%; Score 21; DB 1; Length 5; 60.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0502.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: 415-327-2951
                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 60.v.
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 amino acids
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
STRANDEDNESS: Sin
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1 LDPRP 5
                                                                                           4 MDPTP 8
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1 LDPRP 5
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US-08-335-198-20
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Gaps
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Sequence 68, Application US/07789184

Patent No. 5688768

GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBONGUH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
CORRESPONDENCE MORRISON & FOERSTER
COUNTRY: USA
ZIP: Palo All On All 18 Road
CUNTRY: USA
ZIP: Palo All 1018
COMPUTER READBALE FORM:
COMPUTER READBALE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CLASSIFICATION NUMBER: US/07/789,184
FILING DATE: 19911107
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1e+05;
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                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                    APPLICALLO...
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648205
FILING DATE: 01-0AN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
; REPERENCE/DOCKET NUMBER: 31,284
; REPERENCE/DOCKET NUMBER: 114(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:

ZIP: 30309-4539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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us-10-047-945-7.closed.rai

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Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abus...
STREET: 755 CCTY: Palo Alto
CITY: Palo Alto
California
                                                                                                                                                                                                                                           STREET: 755 Page N
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 MDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-485-886-68
                                              JS-08-485-886-68
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                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-475-263-68
; Sequence 68, Application US/08475263
; Patent No. 575994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
ITILE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: DC
COUTRY: USA
COUTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                            Score 21; DB 1; Pred. No. 4.1e+05;
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415) 813-5600
TELEPHONE: 415) 494-0792
TELEPK: 415) 494-0792
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STARBEDENES: single
                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE KATE H.
REGISTRATION NUMBER: 29,959
REPERRNCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEFRONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEF FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                             48.8%;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | |
LDPRP 5
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                                                                                                                                                                                                                                                                                                                                  4 MDPTP 8
                                                                                                                                                                                                                                                                                                                                                                     1 LDPRP 5
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TOPOLOGY:
US-08-475-263-68
                                                                                                                                                                                                                        US-07-789-184-68
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Sequence 67, Application Us/0848586

PERCENT OF THE CONTROLL SHAIN R.

APPLICANT: CONTROLL SHAIN R.

APPLICANT: CONTROLL SHAIN R.

APPLICANT: CONTROLL SHAIN R.

TITLE OF INVENTION: RELATED PHARMACEUTICALS

CONTROLL ADDRESSER: ADDRESS: ADDRESSER: ADDRESS
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Search completed: May 26, 2005, 20:45:44 Job time : 42 secs
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                      LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-477-134-68
           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        Query Match
Best Local Similarity
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; TOPOLOGY: linear
US-08-473-489A-68
                                                                                                                                                                                                                                                                               4 MDPTP 8
                                                                                                                                                                                                                                                                                                            :|| |
1 LDPRP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 68, Application US/08477134
Patent No. 5856448
Patent No. 5856448
Patent No. 5856448

APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RELATED PHARMACEUTICALS
INVENTION: RELATED PHARMACEUTICALS
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,362
FILING DATE: 07-JUN-1995
CLASSIPICATION: 435
PRICK APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTCRNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEPAX: (415) 494-0792
TELEPAX: (415) 494-0792
TELEPAX: (415) 494-0792
TELEFAX: 34-0154
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LEMGTH: 5 amino acid
TYPE: amino acid
TYPE: AMINO acid
STRANDEDNESS: single
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MEDIUM TYPE: RIOPLY disk
COMPUTER: IRADABLE FORM:
MEDIUM TYPE: RIOPLY disk
COMPUTER: IRA PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-UVN-1995
CLASSIFICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, KATE H.
REGISTRATION NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFREE (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 755 Page Mi
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 MDPTP 8
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1 LOPRP 5
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCAREGROUGH, ROBERT M.
APPLICANT: SCAREGROUGH, ROBERT M.
TITLE OF INVENTION: RELATED PHARMACEUTICALS
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSEE:
APPLICATION DATA:
APPLICATION NUMBER: US/07/789,184
FILING DATE:
CLASSIFICATION NUMBER: US/07/789,184
FILING DATE:
APPLICATION NUMBER: US/07/789,184
FILING DATE:
ATORIEST ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 3; Length 5; Pred. No. 4.1e+05; 1; Mismatches 1; Indels
48.8%; Score 21; DB 2; Length 5; 60.0%; Pred. No. 4.1e+05;
                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-473-489A-68
; Sequence 68, Application US/08473489A
; Patent No. 6024936
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TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELERX: 34-0154
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0%;
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                                                                                           3; Conservative
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Tue May 31 05:57:55 2005

- protein search, using sw model OM protein

May 26, 2005, 18:26:23 ; Search time 15.8 Seconds (without alignments) 60.897 Million cell updates/sec Run on:

US-10-047-945-1 54 1 LKAMDPTPPL 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

8 8 8 Minimum I Maximum I

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* 1: pir1:* Database

2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		di			SUMMARIES	
	Score	Query	Length	DB	ID	Description
-	42	77.8	398	:	A81717	conserved hypothet
2	38	70.4	792	~	T29187	hypothetical prote
m	38	70.4			S62497	
4	37	68.5			AE1681	similar o transcri
2	37	68.5	212		C87585	hypothetical prote
9	37	68.5	237		A42013	alpha-1-B-glycopro
7	37	68.5	286		S72384	hypothetical prote
80	37	68.5	429		809852	hypothetical prote
6	37	68.5	450		B47265	tailless (tll) pro
10	37	æ	452		A35602	tailless (tll) pro
11	37	68.5	1819	7	T32008	hypothetical prote
12	36	66.7	117	7	AF3319	~
13	36	66.7	222	~	C71955	-
14	36	66.7		~	F87552	dprA protein [impo
15		66.7	392	7	T29519	
16	36	66.7		7	T29716	hypothetical prote
17	36	66.7	460	~	H70986	О
18	36	66.7	490	~	T49096	hypothetical prote
19	36	66.7	898	~	T21179	hypothetical prote
20		66.7	944	7	A89624	_
21		66.7	968	~	T46568	ATP-dependent RNA
22	36	66.7	2717	~	A34203	DNA-binding protei
23	35	64.8	159	~	S61040	probable membrane
24	35	64.8	206	N	S50913	TAF25 protein - ye
25	32	•	262	0	E64679	tryptophan synthas
26	35	64.8	291	N	AH2017	lipoic acid synthe
27	35		313	~	A95859	conserved hypothet
28	35	64.8	323	-	TVMVF6	protein kinase (EC
29	35	64.8	380	н	TVFVMM	protein kinase (EC

protein kinase (BC	protein kinase (EC	probable protein k	cytochrome P450-EF	succinate dehydrog	protein kinase (EC	hypothetical prote	protein kinase raf	protein kinase raf	protein kinase raf	beta-glucuronidase	protein p84 - huma	.probable vacuolar	chitinase - Strept	immediate-early pr	hypothetical prote
TVBEG1	TVBEKA	T42612	A53790	I40849	TVRTRR	T18772	S00644	TVHUF6	TVRTRF	A25047	A53545	T50256	T35719	EDBEXD	T46354
П	-	N	~	~	-	~	н	-	ч	~	~	~	~	-	0
382	382	384	543	587	602	627	647	648	648	648	657	678	765	825	1397
80	8	8	œ	æ	8	8	æ	8	æ	æ	ω.	ω.	æ	æ	89.
64.8	64	64	64	64.8	64	64	64	64	64	64	64	64	64	64	64
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	1
	TC0306 [imported]
	TC0306
	l protein
	erved hypothetical
1 11	erved

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

Chlamydia muridarum (strain Nigg)

C;Accession: A81717 C;Accession: A81717 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-398 <TETA;Arsaidues: 1-398 <TETA;Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
A;Experimental source: strain Nigg (MoPn)
C;Genetics:

A;Gene: TC0306 C;Superfamily: Chlamydia trachomatis hypothetical protein CT036

ö Length 398; 77.8%; Score 42; DB 2; 77.8%; Pred. No. 8.4; Pred. No. 8.4; 1; Mismatches Local Similarity nes 7; Conserv Query Match Best Loc Matches

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Gaps

1; Indels Conservative 2 KAMDPIPPL 10 ઠે

| :|||||| KELDPTPPL 317

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Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29187
R;Woossne, J: Stellyes, L.
R;Woossne, J: Stellyes, L.
A;Description: The sequence of C. elegans cosmid C55C3.
A;Reference number: 220585 hypothetical protein C55C3.3 - Caenorhabditis elegans

A;Residues: 1-792 <WOE> A;Cross-references: EMBL:U53335; PIDN:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3 A;Experimental source: strain Bristol N2; clone C55C3 A;Accession: T29187 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

C;Genetics:

A; Gene: CESP: C55C3.3

A;Map position: 4 A;Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43

Query Match

Length 792; 70.4%; Score 38; DB 2;

05:57:55 2005

Tue May 31

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Cyaccesion: G87585

Cyaccesion: G87585

Cyaccesion: G87585

Ryinternan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Nall. Acad. Sci. US.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-1-B-glycoprotein - North American opossum (fragments)
Cypecies: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
C;Date: 10-11992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricatanese, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from oppossum serum of a metalloproteinase inhibitor homologous to hum
A;Reference number: A42013; MUID:92118834; PMID:1731898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nypothetical protein 8 precursor - Enterococcus faecalis plasmid pAD1
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Accession: 572384
R;Hirt, H.; Wirth, R.; Muscholl, A.
R;Hirt, H.; Wirth, R.; Muscholl, A.
R;Hirt, E. Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: A;Reference number: 872375; MUID:97074879; PMID:8917306
A;Reference number: arging sequence not shown; translation not shown
A;Reference number: branch sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9A4W1; GB:AE005673; NID:g13424303; PIDN:AAK24679.1; GSPDB:C
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                                                                                                                                                                                                                                                                          hypothetical protein CC2714 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2; Length 212;
Pred. No. 32;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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A,Molecule type: mRNA
A,Resieus: 1-23 < CAT>
A,CCOSS-references: UNIPROT:Q28359; GB:J05356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 80.0
Matches 8; Conservative
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                                                      130 LKEMDPTKP 138
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Best Local Similarity
Matches 5; Conserv
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CC2714
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C;Decies: Listeria innocua
C;Decies: Listeria innocua
C;Decies: Listeria innocua
C;Decies: Listeria innocua
C;Decession: AE1681
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
S; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;References: UNIPROT:Q92AD1; GB:AL592022; PIDN:CAC97221.1; PID:g16414492; GSPDB:G
C;Genetics:
C;Genetics:
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: liniasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S62497
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1325 <NIB>
A;Cross-references: UNIPROT:Q09847; EMBL:Z64354; NID:g1039338; PIDN:CAA91241.1; PID:g103
B;Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: 221783
A;Reference number: 221783
A;Accession: T38281
A;Accession: T38281
A;Accession: T38281
A;Accession: T38281
A;Accession: T38281
A;Molecule type: DNA
A;Residues: 1-1325 <NI2>
A;Cross-references: EMBL:Z64354; PIDN:CAA91241.1; GSPDB:GN00066; SPDB:SPAC23D3.06c
A;Experimental source: strain 972h-; cosmid c23D3
A;Genetics:
A;Genetics:
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetic
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                                                                                                                                                                                                                                                                                                                                                                  probable nucleoporin - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62497; T38281
R;Niblett, D.; Harris, D.
B;Niblett, D. Harris, D.
A;Reference number: S62492
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                                                 Indels
                                                 1;
        Pred. No. 93;
0; Mismatches
87.5%;
                                             7; Conservative
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    Best Local Similarity
Matches 7; Conserv
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Lailess (tll) protein - fruit fly (Drosophila melanogaster)
NyAlternate names: steroid hormone receptor homolog tll; transcription factor tll
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cipate: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
CiAccession: A35602; A47265
Ripinoni, F.; Baldarelli, R.M.; Steingrimsson, E.; Diaz, R.J.; Patapoutian, A.; Merriam A;File: The Drosophila gene tailless is expressed at the embryonic termini and is a mem A;Reference number: A35602; MUID:90304905; PMID:2364433
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A;Molecule type: DNA
A;Residues: 1-1819 < DAV>
A;Residues: 1-1819 < DAV>
A;Cross-references: UNIPROT:O16625; EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone K10G6
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A;Cross-references: GB:AF019362; GB:L04954; NID:g2429340; PIDN:AAB71371.1; PID:g2440022
A;Note: sequence extracted from NCBI backbone (NCBIN:124057, NCBIP:124058)
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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A.fitle: Characterization of Gownstream elements in a Raf-1 pathway. A;Reference number: A47265; MUID:93157371; PMID:8430097
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A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3
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R;Davidson, S.; Wohldmann, P.; Mullen, G.
submitted to the RMED Data Library, July 1997
A;Bescription: The sequence of C. elegans cosmid KlOG6.
A;Reference number: Z21111
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A;Residues: 1-452 <PIG>
A;Cross-references: UNIPROT:P18102; GB:X52147
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A,Cross-references: PlyBase:FBgn0003720
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216 RALPPTPPL 224
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218 RALPPTPPL 226
                          2 KAMDPTPPL 10
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C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Accession: 509852
E;Accession: 509862
E;Accession: 50
A;Residues: 1-286 <hr/>
A;Crose-references: UNIPROT:Q47791; EMBL:X96977; NID:g1279406; PIDN:CAA65667.1; PID:g127
A;Experimental source: strain OGIX
A;Experimental source: strain OGIX
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics: A;Geneme: plasmid pADI
C;Superfamily: probable pheromone-responsive protein
F:1-26/Domain: signal sequence #status predicted <SIG>F;27-286/Product: hypothetical protein 8 #status predicted <MAT>
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C;Species: Drosophila virilis
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: B47265
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A;Title: Characterization of downstream elements in a Raf-1 pathway.
A;Reference number: A47265; MUID:93157371; PMID:8430097
A;Accession: B47265
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Pred. No. 44;
1; Mismatches 2; Indels
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C;Superfamily: erbA transforming protein homology
C;Keywords: zinc finger
F;32-339/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 1
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A;Molecule type: DNA
Residues: 1-450 <LIA>
A;Cross-references: GB:L04955
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A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A. Reference number: AD3252; PMID:1175688
A. Accession: AF319
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-117 < KUR>
A. Residues: 1-117 < KUR>
A. Experimental source: strain 16M
C. Genetics: BME10540.
A. Map position: I
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RiAlm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; J. Tves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A1800; MUD:99120557; PMID:9923682
A; Accession: C71955
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-222 < ARN>
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A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0241
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Ca.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87552
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B;Nierman, W.C.; Peldblyum, T.V.; Paulsen, I.T.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
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Variety: strain J99
Jate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                       Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                 hypothetical protein BMEI0540 [imported] - Brucella melitensis (strain 16M)
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUD:21173698; PMID:11259647
A;Accession: F87552
A;Status: preliminary
A;Molecule type: DNA
A;Mosicule type: DNA
A;Residues: 1.365 <STO>
A;Residues: 1.365 <STO>
A;Cross-references: UNIPROT:Q9A5K0; GB:AE005673; NID:g13423992; PIDN:AAK24418.1; GSPDB:GCG;Genetics:
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A;Cross-references: UNIPROT:Q23048; EMBL:U64856; PIDN:AAB04987.1; GSPDB:GN00023; CESP:T2|
A;Experimental source: strain Bristol N2; clone T25F10
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Map position: 5
A;Introns: 38/3; 84/2; 156/3; 182/3; 228/3; 256/1; 312/2; 337/3; 361/2
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submitted to the EMBi Data Library, July 1996
A;Description: The sequence of C. elegans cosmid T25F10.
A;Reference number: 220634
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A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0; Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.; "Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae."; Toxicon 32:1237-1249(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                             OPTR78 PRELIMINARY; PRT; 17 AA.

O9TR78;

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-MAY-2001 (TrEMBLrel. 13, Last sequence update)

O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)

ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment).

Blidelphis marsupialis (Southern opossum).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Metaheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
Q67pt6
Q8kud2
Q838g9
Q83g9
Q9f1f9
Q9f1f9
Q9f1f9
Q6hyx5
Q6hyx5
Q6nay5
Q7m6k3
Q7m6k3
Q7m6k3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 2; Length 17; Pred. No. 0.017; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB55FB40E73B2A2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Union metalloproteinase inhibitor DM43.
Didelphis marsupialis (Southern opossum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 AA.
                                                                                                                                                                                                                                             ALIGNMENTS
              Q8KUD2
Q838G9
Q97791
Q9F1F9
Q82YS6
Q84YX5
Q8MYX5
Q70J80
UL88_HCMVA
                                                                                                                                                   Q7M6K3
TLL DROVI
TLL DROME
Q7RV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1947 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
    LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 AA;
 NCBI_TaxID=9268;
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Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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Best Local Similarity 77.8-
Lan 7; Conservative
                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKAMDPTPRL 10
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
                 NCBI_TaxID=9267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y306 CHLMU
Q9PL02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Query Match
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 OC REAL BRIEF BRIE
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha 1B glycoprotein DVOP51-D (Fragment).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidee; Didelphis.
                                                                                                       (Potential) (Potential)
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                                    NOTE-Ref.1.
-!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IPR007110; Ig-like.
InterPro; IPR011015; LEM_like.
                 MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 1; Length 291;
Pred. No. 0.4;
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Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AYIJI000; AAN06911.1; -.
HSSP, 076036; 10LL.
                                                                                                                                                                                                                                                                                                                                                 linked (GlcNAc. . .) (Pc 17A496227E69A65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15297 MW; E19D071A76AA5A7F CRC64;
                                                                                                                                                                                                                                                                                                                 (GlcNAc. ..)
                                                                                                                                                                                                                                                                                              N-linked (GlcNAc. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                               Ig-like V-type 1.
Ig-like V-type 2.
Ig-like V-type 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                               N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                 N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                  32390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LKAMDPTPPL 10
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42 LKAMDPTPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 AA;
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                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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NON TER
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                                                                                                                                                                                                                     DOMAIN
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08HZ74
1D 08HZ
AC 01-M
DT 01-M
DT 01-M
DT 01-M
OS Alph
OS Bide
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Q8HZ75
SPITIFFFFFFFF
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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MEDLINB=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
Dodson R.J., Gayinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
MCClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bacceria, Chlamydiae; Chlamydiales, Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                           Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX131001; AAN06912.1; -.
HSSP, QBNHL6; 1GOX.
InterPro; IPR001599; IG.
InterPro; IPR007110; IG-like.
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TRANSMEM 31 51
                                                                                                                                                                                                                                                                                                           291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
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Pred. No. 66;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40, Last sequence update)
45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 2
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 AA
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Nucleic Acids Res. 28:1397-1406(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                 83.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein TC0306.
OrderedLocusNames=TC0306;
                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
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Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=284590;
                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sed[50007245 Saccharomyces cerevisiae YLL018ca COX19.
ORFNames=KLLA0D03971g;
Kluyveromyces lactis NRRL Y-1140.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR382124; CAH00338.1; -. InterPro; IPR010625; CHCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 AA; 11050 MW; 032BA5DD3C50CAC2 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                    99 AA.
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1; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, C;
01-MAY-2000 (TrEMBLrel. 13, L;
25-OCT-2004 (TrEMBLrel. 28, L;
CG2147-PA (LP02728P).
ORFNAMES=CG2147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.8
hes 7; Conservative
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                              309 KELDPTPPL 317
                   2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 430:35-44(2004)
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LKALSPTPP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF06747; CHCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=NRRE Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope;
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                                                                                                                                                                                                                             Q6CS47;
                                                                                                                                                                                                    Q6CS47
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Matches
                                                                                                                                                RESULT 6
Q6CS47
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Q9W3H5
AC Q9W3H5
AC Q9W3H0
DT 01-M
DT 25-00
DE CG21.
CG2 Drost
CC EUkar
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LKALDPSDPL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=k10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q73ZB2
Q73ZB2;
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0961D3
1D 0961D
DT 01-DE
DT 01-DE
DT 01-DE
DE NAMA1
GN NAMO
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MEDILINE-2259566; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Mixanda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Ebbatta A. (Persons) to the EMBL/GenBank/DDBJ databases.
EMBL; AR063722; AAL39867.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacteriophage Bxzl.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=205877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.2%; Score 39; DB 2; Length 98; 75.0%; Pred. No. 45;
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                                                                                                                          Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                 FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIYBASE, FBGN0030025; CG2147.
SEQUENCE 165 AA, 17157 MW; CF3E6D2E102302C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Origins of highly mosaic mycobacteriophage genomes."; cell 113:171-182(2003).
EBBL; AY129337; AAN16740.1; -
SEQUENCE 98 AA; 10867 MW; D1D8FE87C4CDD15E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
      Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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1 MDPTPPL 7
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                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ntAct; Q9W3H5; -
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QBMLX6
ID QBMLX
AC QBMLX
DT 01-00
DT 01-00
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DT CO
DT C
   REPRESENTATION OF STANTARY STA
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                                                                                                                                                                                                                                                                    "Molecular cloning of a vaccine antigen against infection with the larval stage of Echinococcus multilocularis.";
Infect. Immun. 70:3969-3972 (2002).
EMBL; AX062920; AAL51153.1; -..
EMBL; AX062921; AAL51153.1; -..
InterPro; IPR003951; FN III.
InterPro; IPR003957; FN III.
SMART; SM00060; FN3; 1.
PROSITE; PS50863; FN3; 1.
SEQUENCE 156 AA; 17145 MW; F96E940A0D5B731D CRC64;
                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22060722; PubMed=12065546;
DOI=10.1128/IAI.70.7.3969-3972.2002;
Gauci C., Merli M., Muller V., Chow C., Yagi K., Mackenstedt U.,
Lightowlers M.W.;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017233; AAS04008.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
Bacteria, Actinobacteria; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%; Score 39; DB 2; Length 227; 70.0%; Pred. No. 1.2e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
                                       Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
NCBI_TaxID=6211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
KIAA1115 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%; Score 39; DB 2; 70.0%; Pred. No. 76; iive 2; Mismatches
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EM95 vaccine antigen.
Echinococcus multilocularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
OrderedLocusNames=MAP1691c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 70.0
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146 LAALDPRPPL 155
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Name=SPV074;
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                                                                                                  Straubberg R.L., Feingeld E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,
Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Krzyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Krzyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pubmed=1521079; DOI=10.1073pnas.0305659101; Pubmed=1521079; DOI=10.1073pnas.0305659101; Pubmed=1521079; DOI=10.1073pnas.0305659101; Pubmed W. Krank A.C., Karlberg B.O., Legault B.-A., Ardell D.H., Canbaeck B., Eriksson A.-S., Naselund A.K., Handley S.A., Huvet M., La Scola B., Holmberg M., Andersson S.G.B.; "The louse-borne human pathogen Bartonella quintana is a genomic derivative of the zoonoric agent Bartonella henselae."; Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

EMBL; BX897699; CAF28391.1; -...
GO; GO:0008152; Firmansferase activity; IEA.
GO; GO:0008152; Pimetabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                         TISSUB=Placenta;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-plsC; OrderedLocusNames=BH16290;
Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007629; AAH07629.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AA; 24559 MW; 9094604DE4A93228 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.2%; Score 39; DB 2; 1 66.7%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-acyl-sn-glycerol-3-phosphate acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0010,1.v.,
GO; GO:0008152; P:metabollusu, --
InterPro; IPR002123; Acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 49882 / Houston 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:: |||||
130 LRSQDPTPP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=38323;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swinepox virus (SWPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                              Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 320;
                                                                                        Score 39; DB 2; Length 200
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0006265; P:DNA topological change; IEA.
GO; GO:0006268; P:DNA unwinding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Pfam; PF01553; Acyltranaferase; 1.
SMART; SM00563; PlaC; 1.
Acyltranaferase; Complete proteome; Tranaferase.
SEQUENCE 268 AA; 30957 MW; 2P955B7EBFBDBB95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 AA; 38179 MW; 97P9B94442DD1DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2; I
Pred. No. 1.7e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                 320 AA.
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                                                                                                                72.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match
Best Local Similarity 50.0%,
S. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPV074 DNA topoisomerase.
                                                                                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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241 IKSLDPVPPI 250
                                                                                                                                                                                                                                                   240 LAAQDPTPP 248
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                                                                                                                                                                                                       1 LKAMDPTPP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
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NCBI_TaxID=10276;
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Search completed: May 26, 2005, 18:43:17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 6:197-205(1999).
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Gbrown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K.M., Ruters S., Seeger K., Saunders D., Shary S., Squares R., Squares S., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                             'Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 39; DB 2; Length 693; 70.0%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75941 MW; E54676BCCA33A921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09UPN7; 09BU97;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Hydrolase.
SEQUENCE 693 AA; 75941 MW:
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:||| |:
420 LKALDPTRPV 429
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                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
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RA15, HUMAN

TO 28-PEB

DT 28-PEB
          KARARA KA
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez R.M., Schimwood J., Schmutz J., Myers R.M., Schimwood J., Schmutz J., Myers R.M., Schein J.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 4.4e+02;
2; Mismatches 1; Indels
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Poly-Glu.
P -> S (in Ref. 1).
9 B86964AE2226774E CRC64;
                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-1690:
-!- SIMILARITY: Belongs to the SAPS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glu-rich.
Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB029038; BAA83067.2; ALT_INIT.
EMBL; BC002799; AAH02799.1; -.
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751 P3
504 P6
558 P6
751 P
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Genew, HGNC:29195; KIAA1115.
InterPro; IPR007587; SAPS.
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nes 6; Conservative
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DOMAIN
CONFLICT
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May 26, 2005, 18:17:22 ; Search time 86 Seconds (without alignments) 44.972 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           - protein search, using sw model
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2105692 Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-047-945-1 54 1 LKAMDPTPPL 10 Perfect score: Scoring table: Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 seq sed 88 Minimum 1 Maximum 1

geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A_Geneseq_16Dec04: geneseqp2002s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	Score	Query Match	Length DB	DB	ID	Description	
	54	100.0	10		AAW53843	Aaw53843 N-terminu	rminu
7	54	100.0	10	7	ABB80222	Abb80222 Syntheti	netic
٣	54	100.0	11	7	ABB80226		netic
4	54	100.0	12	7	ABB80225	Abb80225 Syntheti	netic
S	54	100.0	15	?	AAW11575	Aaw11575 N-termina	rmina
9	54	100.0	15	~	AAW53841		rminu
7	54	100.0	15	7	ABB80223	Abb80223 Synthetic	netic
80	20	95.6	6	1	ABB80227	Abb80227 Synthetic	netic
6	43	79.6	æ	7	ABB80228	Abb80228 Synthetic	netic
10	42	77.8	94	4	AA002179	Aao02179 Human pol	lod r
11	41	75.9	165	4,	ABB58900	Abb58900 Drosophi	phil
12	39	72.2	459	m	AAB59012	Aab59012 Breast	st an
13	39	72.2	754	œ	ABM82174	Abm82174 Tumou	Tumour-as
14	39	72.2	754	œ	ADS88328	Ads88328 Human	Human pro
15	38	70.4	78	4	AAM85892	-	n imm
16	38	70.4	108	7	ABM74107	Abm74107 DNA C	DNA clone
17	38	70.4	267	7	AAY43943	Aay43943 Yeast	: pro
18	38	70.4	349	m	AAG17097	Aag17097 Arabidops	idops
19	38	70.4	369	ო	AAG47069		Arabidops
20	38	70.4	369	ო	AAG24233		Arabidops
21	38	70.4	369	ស	ABB93666	-	icida
22	38	70.4	405	m	AAG47028	Aag47028 Arabidops	idops
23	37	68.5	15	N	AAW39043	Aaw39043 Peptide	ide r
24	37	-:	210	~	AAY00125	Aay00125 Enterococ	rococ
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ABU88372 ABU13623 AAY00124 AAY00124 ABV931313623 ABU136194 ABU2994 ADH88791 ADH88791 ADH88791 ADH85164 ADH85164 ADH85164 ABG17160 ADF60462 AA006147 ABG3279	AAW55552 ABO67138
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<u>4</u> 4. 4 ቢ

## ALIGNMENTS

LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment. AAW53843 standard; peptide; 10 AA. N-terminus of opossum LINF. (first entry) 08-JUL-1998 AAW53843; AAW53843 

Didelphis virginiana US5744449-A. 28-APR-1998.

96US-00657163. 93US-00058387. 03-JUN-1996; 10-MAY-1993; 22-SEP-1994;

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps FW, Lipps BV; WPI; 1998-271108/24. Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.

Claim 7; Col 11; 11pp; English.

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

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Sequence 11 AA;
                                                             Matches
                                                                                                                                                RESULT 3
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snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                          Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 19E; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                      Length 10;
                                                                                                0; Indels
                                                                        Score 54; DB 2;
Pred. No. 0.033;
                                                                                                 0; Mismatches
                                                                                                                                                                                                          ABB80222 standard; peptide; 10 AA
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                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-2002; 2002US-00047945.
                                                                                                                                                                                                                                                            (first entry)
                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                              LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                    Synthetic LTNF, LT-10.
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                                                                                                                        1 LKAMDPTPPL
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                        to horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003060471-A2.
                                                Sequence 10 AA;
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saliva; ELISA
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and tracular, the methods of the invention are useful for diagnosing and abbetes, autoimmune disease (a.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva callection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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0
                                                                 100.0%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                    1 LKAMDPTPPL 10
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                                                                     Query Match
Best Local Similarity
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Sequence 10 AA;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, atthritis, Sjogren's syndrome, Reiter's syndrome of season or hedgin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifiged immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                                               IGB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                             Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clotting time before centrifugation to separate serum. Saliva proteins
                                       Gaps
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                                       ö
 Length 11;
                                     0; Indels
100.0%; Score 54; DB 7; 100.0%; Pred. No. 0.036;
                                     Mismatches
                                                                                                                                                                                              ABB80225 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                       (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                     1 LKAMDPTPPL 10
                                                                                           Synthetic LTNF, LT-12
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LIPPS F W.
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The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity to the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
                                                                                                                                                                                                                                   Lethal toxin neutralising factor, LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
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                                                                                                                                                                            (first entry)
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LKAMDPTPPL 10
                           LKAMDPTPPL 10
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                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                Didelphis virginiana.
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                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1994;
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20-MAR-1997
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                                                                                      AAW11575
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Gaps

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100.0%; Score 54; DB 7; Length 12; 100.0%; Pred. No. 0.039; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 10; Conservative

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (IgE), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva con tentifugation to separate serum. Saliva proteins collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 3; 24pp; English.
                                                                                                                                                                              14-JAN-2003; 2003WO-US001044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Blapidee, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                              LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy, anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
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94US-00310340
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N-terminus of opossum LINF.
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RESULT 7 ABB80223

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                                                                                                                                                     Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
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                       14-JAN-2003; 2003WO-US001044
                                              14-JAN-2002; 2002US-00047945
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9; Conservative
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                                                                                                                               WPI; 2003-636703/60.
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24-JUL-2003
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addisease or Hödgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva callection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 4; 24pp; English.
14-JAN-2002; 2002US-00047945.
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18-MAY-2000; 2000US-00577409.
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                                                                  (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Length 165; 0; Indels

Tang YT,

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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cycostatic; immunosuppressive; nootropic, neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast and ovarian cancer associated antigen protein sequence SEQ ID 720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                               75.9%; Score 41; DB 4;
100.0%; Pred. No. 73;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1174-1176; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59012 standard; protein; 459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-611515/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                4 MDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDPTPPL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF21915.
                                                                                                                                                                                                                                                                               Sequence 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200055173-A1.
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            886666666668888
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                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nemantopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                               Claim 20; SEQ ID NO 16071; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 4
Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB58900 standard; protein; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWD,
                                      Drmanac RT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 ĽKSQDPTPP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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                                                                                 2001-514838/56.
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N-PSDB; ABL03003.
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                                   Liu C,
                                                                                                          N-PSDB; AAI82110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94 AA;
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treatment

27-SEP-2001

ABB58900;

RESULT 11 ABB58900

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antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anamia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatorid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide acquences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour-associated antigenic target (TAT) polypeptide PRO83096, SEQ:5611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor-associated antigenic target polypeptides and nucleic acids, ful in preparing a medicament for treating or detecting a liferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                             Length 459;
                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                           Score 39; DB 3; I
Pred. No. 4.3e+02;
; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM82174 standard; protein; 754 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                              346 LRSQDPTPP 354
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                                                                                                                                                                                                                                                                                                                                                       1 LKAMDPTPP 9
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                                                                                                                                                                                                   infectious diseases
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACN40680
                                                                                                                                                                                                                                       Sequence 459 AA;
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                                                         antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, luga cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, ovarian cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha (TNF-alpha) -signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein of a TNF-alpha signalling pathway protein complex Seq 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
molecule which binds to a TAT polypeptide; fusion proteins comprising TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                          Length 754;
                                                                                                                                                                                                                                                                                                          Score 39; DB 8; I
Pred. No. 7.1e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS88328 standard; protein; 754 AA.
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                                                                                                                                                                                                                                                                                                          72.2%;
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10-FEB-2003; 2003EP-00100274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 641 LRSQDPTPP 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases or cancer.
                                                                                                                                                                                                                                                                                                                                                                                           1 LKAMDPTPP
                                                                                                                                                                                                                                                                  Sequence 754 AA;
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2000US-0237040P
2000US-0239935P
2000US-024121P
2000US-024121P
2000US-0241786P
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2000US-0241786P
2000US-024186P
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             rheumatoid arthritis and inflammatory bowel disease; infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirhematic, cytostaric and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway
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Pred. No. 7.1e+02;
2; Mismatches 1; Indels
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Matches 6; Conservative
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641 LRSQDPTPP 649
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19-MAY-2000; 2
07-JUN-2000; 2
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Search completed: May 26, 2005, 18:36:48
Job time : 90 secs
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ANK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cuplynucleotides may be used to produce the secreted (I), by inscrting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AK64703
cancers and cancer metastases of haematopoietic-derived cells. AK64703
to AAK89694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK8950 and AAM82169
represent sequences used in the exemplification of the present invention Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. Claim 11; SEQ ID NO 13485; 3071pp + Sequence Listing; English.

Gaps ö 70.4%; Score 38; DB 4; Length 78; 70.0%; Pred. No. 1.18+02; ive 1; Mismatches 2; Indels Query Match
Best Local Similarity 70.0
Matches 7; Conservative

1 LKAMDPTPPL 10

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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
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                            Sequence 1, Application US/10047945

Publication No. US200301575531

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIPPS, BINE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FILING DATE:
CURRENT FILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO!
TYPE: PRI
TYPE
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CTHER INFORMATION: US 5,576,297.
US-10-047-945-1
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Matches 10; Conservative
US-10-047-945-1
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SEQ ID NO 6
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                               Sequence 5, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATON: (19E) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
PRIOR PLILING DATE: 2002-01-14
PRIOR FILING DATE: 1 FOR WINDOWS
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Seduence 4. Application US/10047945

GENERAL INFORMATION: US20030157555A1

APPLICANT: LIPPS, BINIE V.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1gE)/IMPLICATED DISORDERS
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Pred. No. 0.062;
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CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO L
LENGTH: 12
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11 Similarity 100.0%;
10; Conservative 0
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Best Local Similarity
RESULT 2
US-10-047-945-5
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LENGTH: 11
TYPE: PRT
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US-10-047-945-4
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RESULT 4 US-10-047-945-2 ; Sequence 2, Application US/10047945

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) Publication No. US20030157555A1
) GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PELING DATE:
NUMBER OF REATH OF THE CONTROL OF
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Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN ITILE OF INVENTION: LIPPSINGS INSTITUTION UNMERS: US/10/047,945
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR PILING DATE: 2002-01-14
PRIOR FILING DATE:
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Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50; DB 14; 1
Pred. No. 1.3e+06;
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7, Application US/10047945; Publication No. US20030157555A1; GENERAL INFORMATION:
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OTHER INFORMATION: US 5,576,297.
US-10-047-945-2
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; OTHER INFORMATION: Synthetic.
US-10-047-945-6
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-047-945-7
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162813
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US-10-437-963-162813
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OTHER INFORMATION: unbure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.9
Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 6; Conservat
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42 LRAREPTPPL
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APPLICANT:
APPLICANT:
APPLICANT:
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: ADAU Yihua
APPLICANT: Car Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 253125
LENGTH: 80
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70598C.1.pep
US-10-424-599-253125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.9%; Score 41; DB 15;
70.0%; Pred. No. 45;
tive 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 133945, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
; OTHER INFORMATION: Synthetic.
US-10-047-945-7
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.6
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                 LENGTH:
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RESULT 13
US-10-767-701-51220
US-10-767-701-51220
Sequence 51220, Application US/10767701
Sequence 51220, Application US/10767701
Sequence 51220, Application No. US20040172684A1
Sequence 51220
Sequence 51220, Application US/10767701
Sequence 51220
Sequence 5122
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-720
                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PAIOSPICI
CURRENT APPLICATION: NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR PELICATION NUMBER: PCT/US00/05881
PRIOR PELICATION NUMBER: PCT/US00/05881
PRIOR PELICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver: 2.0
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Pred. No. 5.1e+02;
2; Mismatches 1; Indels
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Pred, No. 1.2e+02;
0; Mismatches 2; Indels
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US-10-767-701-51220
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Sequence 720, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.4%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 77.87
Local 7; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 LRSQDPTPP 354
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
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LENGTH: 75
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    APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Youngei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Birbaruk, Brad

APPLICANT: Li, Ping

APPLICANT: NUMBER: US, 10/437, 963

CURRENT APPLICATION NUMBER: US/10/437, 963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 162816

LENGTH: 206

TOPEL: PRICALLY APPLICATION

TOPET: PRICALLY APPLICATION

TOPEL: PRICALLY APPLICATION

TOPET: PRICA
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; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-720
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Fublication No. US20020039764A1
GENERAL INFORMATION:
FIGHERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO3
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 39; DB 16; Length 206; 60.0%; Pred. No. 2.3e+02; tive 3; Mismatches 1; Indels
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-925-298-720
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Gaps

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RESULT 12 US-10-102-806-720

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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138037
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; Publication No. US20050108791A1
; GENERAL INFORMATION.
; GENERAL INFORMATION.
; APPLICANT: Edgerton, Michael D
; TITLE OF INVERTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-120-10
; PRIOR APPLICATION NUMBER: 10/310,154
; ROOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1996
; LENGTH: 369
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US-10-437-963-138037
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; ORGANISM: Arabidopsis thaliana
US-10-732-923-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.4
Best Local Similarity 60.0
Matches 6; Conservative
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1 MPSQDPTPPL 10
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ORGANISM: Oryza sativa
FEATURE:
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59 KAVEPTPP 66
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US-10-732-923-1996
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LENGTH: 10
TYPE: AMINO ACID
STRANDENESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID
HYPOTHETICAL: NO
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Sequence 1, Appli
Sequence 43223, A
Sequence 442, Appl
Sequence 444, Appl
Sequence 232, Appl
Sequence 232, Appl
Sequence 676, Appl
Sequence 676, Appl
Sequence 13655, Appl
Sequence 166, Appl
Sequence 166, Appl
Sequence 166, Appl
Sequence 12, Appl
Sequence 165, Appl
Sequence 165, Appl
Sequence 165, Appl
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2, Appli
1, Appli
2, Appli
3, Appli
4, Appli
                                                                                                                                 May 26, 2005, 18:29:58 ; Search time 22.8 Seconds (without alignments) 32.741 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                   513545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents AA:*
1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-657-163A-2

US-08-110-340A-1

US-08-210-163A-1

US-09-270-767-43223

US-09-949-016-8760

US-08-5224-44

US-08-50-124-444

US-09-50-124-444

US-09-134-000C-6676

US-09-134-000C-6676

US-09-134-000C-6583

US-09-134-000C-6583

US-09-248-796A-12655

US-09-248-796A-12

US-09-248-796A-12

US-09-248-796A-12

US-08-909-981-12

US-08-909-981-12

US-08-276-151-5

US-08-276-151-5
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US-08-185-282-4
                                                                                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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54
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Match Length DB
                                                                                                                                                                                                                                                                      1 LKAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                     Scoring table:
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Sequence 13, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 16, Appl
Sequence 47, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 31, Appli
Sequence 32, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TASA
COUNTRY: USA
ZIP: 77401
                                ZIP: 77401

ZAP: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: 2.4
PRIOR APPLICATION 5.14
PRIOR APPLICATION NUMBER: 08/310,340
FILING DATE: 2.2 SEPTEMBER 1994
CLASSIFICATION: S14
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
TELERHONE: 713-482-2961
TELERPANE: 713-482-2961
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Gaps
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Sequence 1, Application US/08657163A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BINIB V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 4509 MIMOSA DR.
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 54; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 10; Conservative 0; Mismatches 0; Indels
                     TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD COVERESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREEL 300 MINIOR DELAGES
COUNTY: BELLAIRE
STATE: TEXAS
COUNTY: USA
ZIP: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER. IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: 200 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/310,340
FILING DATE: 10 MAY 1993
APPLICATION NUMBER: 22 SEPTEMBER 1994
CLASSIFICATION NUMBER: 24 SEPTEMBER 1994
CLASSIFICATION NUMBER: 28 SEPTEMBER 1994
CLASSIFICATION NUMBER: 28 1993
APPLICATION NUMBER: 28 1993
APPLICATION NUMBER: 28 1993
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-FAT-US-011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1: ORGANISM: DIDELPHIS VIRGINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
   JONAS PERALES, ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQUENCE 15
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
STRANDEDNESS: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 713-482-290
TELEFAX: 713-663-7290
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                 DATE: 3-8 NOV 1991
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                                                                                                                                                                                                                                                                                                                                                 US-08-310-340A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-657-163A-1
   AUTHORS:
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| Sequence 1, Application US/08310340A
| Sequence 1, S57629;
| Patent No. S57629;
| GENERAL INFORMATION:
| APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
| TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
| TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
| TITLE OF INVENTION: UTLLITY AS TREATMENT FOR ENVENOMATION
| NUMBER OF SEQUENCES: 1
| CORRESPONDENCE ADDRESS: 3
| ADDRESSEE: BINIE V. LIPPS
| STREET: 4509 MIMOSA DR. 3
| CITY: BELLAIRE
| STREET: TEXAS COUNTRY: USA 3
| CITY: USA 4
| CI
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                                                                                                    Query Match 100.0%; Score 54; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0043; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OMPUTER: IBM COMPATIBLE
OFERATING SYSTEME: MS HOSD 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 2 SEPTEMBER 1994
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE: TEXAS V
DEVELOPMENTAL STAGE: ADULT
   SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                1 LKAMDPTPPL 10
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1 LKAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: BLOOD
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: WILD
       ; ORIGINAL SUI
US-08-657-163A-2
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; ORGANISM: Human
US-09-949-016-8760
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                  AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 54; DB 1; Length 15; 100.0%; Pred. No. 0.0066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Xaa means any amino acid US-09-270-767-43223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WI
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL INPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: JONAS PERALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKAMDPTPPL 10
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; PAGES: 104
; DATE: 3-8 NOV 1991
US-08-657-163A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 43223
LENGTH: 253
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Gaps
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Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STRETT: Hadlaubstrasse 151
CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                72.2%; Score 39; DB 4; Length 72; 75.0%; Pred. No. 11; 11; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMOUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFRX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M: Saccharomyces cerevisiae
Protein kinase; Table 8 Column 48
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaetSEQ for Windows Version 4.0
SENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, TITLE: The protein Kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RIMDPIPP 68
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TOPOLOGY: linear
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US-09-071-035-232
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                                         Gaps
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                                                                                                                                                                                                                                                     APPLICANT: SPARS, Andrew B.
APPLICANT: SPARS, Andrew B.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
 DB 2; Length 267;
67;
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                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDLUM TYPE: FIDAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILLING DATE: 16-FEB-1996
CLASSIFICATION: 435
 Score 38; DB 2
Pred. No. 67;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 444:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37;
Pred. No.
                                                                                                                                                                                                    Sequence 444, Application US/08602999A Patent No. 6184205
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Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
   70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.,
Query Match 70.4
Best Local Similarity 70.0
Matches 7; Conservative
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LENGTH: 15 amino acids
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                                                                          1 LKAMDPTPPL 10
                                                                                                 31 LKVVDPTPEL 40
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5 RALPPTPPL 13
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US-08-602-999A-444
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US-09-500-124-444
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Sequence 232, Application US/09071035
Sequence 232, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                           APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CITYE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLIANCE DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistorck, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110.1-20
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
QUILLIAM, Lawrend
DER, Channing J.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60...
6. Conservative
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ADDRESSEE: Pennie &
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5 RALPPTPPL 13
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Gaps

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US-09-134-000C-6676

US-09-134-000C-6676

Sequence 6676, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: BATEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT FELING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 6676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.5%; Score 37; DB 4; Length 306; 66.7%; Pred. No. 1.18+02; rative 1; Mismatches 2; Indels
          DB 4; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.5%; Score 37; DB 4; Length 291
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels
          Score 37; DB Pred. No. 94; 1; Mismatches
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; Sequence 13655, Application US/09489039A
; Patent.No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecalis
          Query Match 68.5%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66...
6. Conservative
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70 KPIDPIPPI 78
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                                                                                                                                                            50 KPTDPTPPI 58
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US-09-134-000C-6583
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Sequence 230, Application US/09071035
Patent No. 644804104:
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CCUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: PB36.373
REFERENCE/DOCKET NUMBER: PB36.97;
TELERPHONE: (301) 309-8504
TELERPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYRNDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                            PB369P2
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CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 98369
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.5
Best Local Similarity 66.7
Matches 6; Conservative
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Search completed: May 26, 2005, 19:08:37 Job time : 24 secs
                      Query Match
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US-09-248-796A-20624

Sequence 20624, Application US/09248796A

Sequence 20624, Application US/09248796A

Sequence 20624, Application US/09248796A

Setting the control of the 
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PREUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13655
LENGTH: 323
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US-09-270-767-57016
US-09-270-767-57016
Sequence 57016, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
UNUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57016
LENGTH: 27
TYPE: PRT
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.7%; Score 36; DB 4; Length 323; Best Local Similarity 77.8%; Pred. No. 1.8e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 KAKDPTDPL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LKAMDALPP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-248-796A-20624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-13655
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                        Gaps
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Score 35; DB 4; Length 27;
Pred. No. 18;
                      1; Indels
                        3; Mismatches
 64.8%;
55.6%;
            Best Local Similarity 55.6
Matches 5; Conservative
                                                            |: :||:||
19 LRPLDPSPP
                                             1 LKAMDPTPP
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GenCore version 5.1.6
Copyright,(C) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2005, 18:26:23 ; Search time 23.7 Seconds (without alignments) 60.897 Million cell updates/sec

1 LKAMDPTPPLWIKTE 15 US-10-047-945-2 84 ritle: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mypothetical protein mannoglobulin-lik probable glycosyl hypothetical protein hydroxymethylgluta hypothetical proteconserved hypothetical protein aspartate transami major structural n fasciclin I precur ribosomal protein exodeoxyribonuclea hypothetical prote probable DNA (cyto C4 protein - tomat micofilarial sheat alpha-1-B-glycopro ypothetical prote two-component sens myocyte enhancer myocyte enhancer probable acyl-CoA lantibiotic Peps Description SUMMARIES Query Match Length DB Result

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two-component resp	probable 2-oxoacid	uncharacterized pr	Xaa-Pro dipeptidas	hypothetical prote	probable beta-gluc	probable membrane	probable protein P	hypothetical prote	mucin MUC5B, trach	dprA protein (impo	probable serine/th	hypothetical prote	28K protein - suid	hypothetical prote	gene 65 protein -
F69977	H72626	A97084	C83867	D86446	T02404	865208	D86387	B70614	T45025	F87552	A57286	AD1928	WMBEPN	T23957	831010
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231	309 2	337 2	406 2	422 2	560 2	609 2	1184 2	1215 2	3570 2	365 2	631 2	242 2	256 1	258 2	268 2
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	47.6 309 2						•	•	۲٠,						
							•	•	۲٠,		47.0	9 46.4			

## ALIGNMENTS

RESULT

A42013	
alpha-1-B-glycoprotein - North American opossum (fragments)	
C; Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu	obossnı
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004	
C;Accession: A42013	
R;Catanese, J.J.; Kress, L.F.	
Biochemistry 31, 410-418, 1992	
A; Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum	to hum
A; Reference number: A42013; MUID:92118834; PMID:1731898	
A; Accession: A42013	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-237 <cat></cat>	
A, Cross-references: UNIPROT: Q28359; GB: J05356	
C;Keywords: glycoprotein	
Query Match 75.0%; Score 63; DB 2; Length 237;	
Dest bocal similarity 00.0%; Fred: NO. 0.0030; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
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LKAMDPTPPLWIKTE 15

TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-1213 <VER> A;Cross-references: UNIPROT:Q24325; GB:X79243; NID:g541664; PIDN:CAA55830.1; PID:g541665 C;Accession: A54063
R;Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.
Science 264, 933-941, 1994
A;Title: Drosophila TAP-II 150: similarity to yeast gene TSM-1 and specific binding to A;Reference number: A54063; MUD:94233377; PMID:8178153
A;Accession: A54063

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A,Gene: FlyBase:Taf150 A,Cross-references: FlyBase:FBgn0011836 C, Genetics:

Gaps ö 19 13; Score 46; DB 2; Length 1213; larity 53.3%; Pred. No. 32; Conservative 3; Mismatches 4; Indels Query Match Best Local Similarity Matches 8; Conserv

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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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A,Molecule type: DNA
A,Residues: 1-687 <STO>
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A,Status: preliminary
A,Molecule type: DNA
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C;Species: Schizosaccharomyces pombe
C;Accession: T38769; T38072
A;Reference number: Z21810
A;Accession: T38769
A;Molecule type: DNA
A;Residues: L105 <GEN
A;Experimental source: strain 972h-; cosmid c3H8
A;Experimental source: strain 972h-; cosmid c3H8
A;Experimental source: strain 972h-; cosmid c3H8
A;Status: translated from GB/EMBL/DDBJ
A;Accession: T38072
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 90-777 <CON>A;Residues: 90-777 <CON>A;Residues: 90-771 <CON>A;Residues: BMBL:Z0690; NID:g1256511; PIDN:CAA94619.1; PID:g3859771; GSPDB:GNGC
A;Experimental source: strain 972h-; cosmid c1F3
C;Genetics:
A;Genetics: A;Genetic
                                      CiSpecies: Pyrococcus abyssi
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
CiAccession: E75099
Ainonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
Ainonymous, Genoscope
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A;Experimental source: strain Orsay
C;Genetics:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T09402
C;Accession: T09402
R;Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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pothetical protein PAB1590 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 2; Length 695;
Pred. No. 36;
3; Mismatches 2; Indels
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212 SVDETEPIWVSTE 224
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561 ANDPKPPMWLE 571
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A, Gene: PAB1590
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A;Accession: T09402
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1327 <maz>
A;Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:g2645889; PIDN:AAC52057.1; PID:g2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Salmonella enterica subsp. enterica servar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB064
R;Parchill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Pickard, D.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow, A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CjAccession: D86314
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Vi, Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.X.; Liu, Z.X.; Maiti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enterica subsp. enterica ser
Genomics 48, 157-162, 1998
A;Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.
A;Reference number: Z16665; MUID:98190514; PMID:9521868
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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Pred. No. 75;
2; Mismatches
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Pred. No. 24;
3; Mismatches
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Gaps

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 «TET>
A;Cross-references: UNIPROT: Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-May-1999 #sequence revision 21-May-1999 #text_change 09-Jul-2004
S,Accession: T04646; S56657; S47490
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Isolation, characterisation and expression of a cDNA clone encoding plastid asp. Reference number: S56657; MUID:95284373; PMID:7766905
Accession: S56657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiRead, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain N1gg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana N/Alternate names: aspartate aminotransferase; protein F10N7.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: aspartate aminotransferase
C;Keywords: aminotransferase; chloroplast; phosphoprotein; pyridoxal phosphate
F;298/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 20/3; 37/3; 102/3; 115/3; 145/3; 182/1; 218/3; 266/3; 322/2; 410/3
A;Note: F10N7.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Chlamydia muridarum, Chlamydia trachomatis Mořn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-21,'NV',24-453 <WIL>
A;Cross-references: EMBL:X81026; NID:9531554; PIDN:CAA56932.1; PID:9531555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Chlamydia trachomatis hypothetical protein CT036
                                              Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P46248; EMBL:ALO21636;Experimental source: cultivar Columbia; BAC clone F10N7;Wilkie, S.E.; Roper, J.M.; Smith, A.G.; Warren, M.J. lant Mol. Biol. 27, 1227-1233, 1995
                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                          Score 42; DB;
Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                       7
                                              50.0%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                6; Conservative
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                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                         97
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                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                             4 MDPTPPLWI
                                                                                                                                                                                                                                                                                         89 ISPSPPLWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,Residues: 1-453 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A81717
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A;Genome: nuclear
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hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrot)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A31898; A28367
C;Accession: A31898; A28367
J: Biold. Chem. 263, 18411-18418, 1988
A;Fitle: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Note: the authors translated the codon GGA for residue 805 as Glu
R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
Biol. Chem. 263, 2513-2517, 1988
A;Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev
A;Reference number: A28367; MUID:88115403; PMID:3276692
A;Rocession: A28367
A;Molecule type: mRNA
A;Residues: 689-735 - WO2>
C;Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t
C;Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
C;Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N
F;279,850,886,930/Binding site: carbohydrate (Asn) (covalent) #status predicted
A,Cross-references: UNIPROT:Q9LMT8; GB:AE005172; NID:g9665069; PIDN:AAF97271.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-932 <MOO>
A;Residues: 1-932 <MOO>
A;Residues: UNIPROT:P16393; GB:J04200; NID:g161522; PIDN:AAA30060.1; PID:g161523
A;Notes: the authors rearranged portions of the coding region in Figure 2, and the above submitted to GenBank
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A;Experimental source: strain OT3
A;Note this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y.; Hino, Y.; Yamamoto, S.; Sekin
Yamazaki, J.; Kushida, N.; Oguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PH1828 - Pyrococcus horikoshii C; Species: Pyrococcus horikoshii C; Species: Pyrococcus horikoshii C; Species: Pyrococcus horikoshii C; Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004 C; Accession: D71194 Ts. Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekii M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, S5-76, 1998 A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A; Reference number: A71000; MUID:98344137; PMID:9679194 A; Accession: D71194 A; Accession: D7194 A; Accession: D7194 A; Accession: D7194 A; Accession: D
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                                                                            A;Map position: 1
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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Pred. No. 73;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                   2; Length 687;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                   DB
52;
                                                                                                                                                                                                                                          51.2%; Score 43; DB 46.7%; Pred. No. 52; tive 3; Mismatches
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Conservative
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298 KKIDPTMPLW 307
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 7; Conserv
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C;Species: Zea mays (maize)
C;Species: Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Jacesion: D: 701-704, 1993
Plant Mol. Biol. 21, 701-704, 1993
Plant Mol. Biol. 21, 701-704, 1993
A;Title: CDNA muclectide sequence and expression of a maize cytoplasmic ribosomal protein A;Reference number: S30146; MUID:93192530; PMID:8448368
                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-151 a.QAA.
A,Residues: 1-151 a.QAA.
A,Cross-references: UNIPROT: Q05761; EMBL:X62455; NID:g288058; PIDN:CAA44311.1; PID:g28801
C,Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology
C,Reywords: protein biosynthesis; ribosome
F;2-151/Product: ribosomal protein S13 #status predicted aMAI>
F;82-148/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myocyte enhancer factor 2B-2 - mouse
myocyte enhancer factor 2B-2 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11.Mar-1998 #sequence_revision 11-Mar-1998 #text_change 09-Jul-2004
C;Accesion: 4C5882
R;Morisaki, T.; Sermsuvitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Morisaki, H.; J. Biochem. 122, 939-946, 1997
J. Biochem. 122, 939-946, 1997
A;Fitle: Mouse Mef2b gene: Unique member of MEF2 gene family.
A;Reference number: 4C5881; MUID:98104045; PMID:9443808
A;Accession: 4C5882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:O55087; DDBJ:D87828
C;Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.8%; Score 41; DB 1; Length 151; 75.0%; Pred. No. 20; ative 1; Mismatches 1; Indels
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Pred. No.
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ribosomal protein S13, cytosolic - maize
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Best Local Similarity 61.57
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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Cjpecies: Schietocerca americana (American bird grasshopper)
R;Zinn, K.; McAllister, L.; Goodman, C.S.
Cell 53, 577-587, 1988
A;Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Drc A;Reference number: A29900; MUD:88223351; PMID:3370670
A;Accession: A29900
A;Status: preliminary
A;Mocelule type: mRNA
A;Residues: 1-62 <ZIN>
A;Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:g160846; PID:g160847
A;Residues: 1-62 <ZIN>
A;Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:g160846; PID:g160847
A;Residues: 1-62 <ZIN>
A;Residues: 1-62 <ZIN>
A;Residues: 1-62 <ZIN-
A;Residues: A31817
A;Molecule type: mRNA
A;Residues: 25-42 <SNO>
A;Cross-references: EMBL:M20544; EMBL:J03787
                                                                                                                                                                                                                                                                                                                                                                                                                Major structural nucleoprotein - Machupo virus

N.Alternate names: nucleocapsid protein

N.Alternate names: nucleocapsid protein

N.Alternate names: nucleocapsid protein

C.Becies: Machupo virus

C.Becies: Machupo virus

C.Accession: S18042

R.Griffiths, C.; Wilson, S.M.; Clegg, J.C.S.

Rubmitted to the EMBL Data Library, October 1991

A.Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship wire

A.Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship wire

A.Molecule type: genomic RNA

A.Molecule type: genomic
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                                                                            Gaps
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Pred. No. 72;
1; Mismatches 4; Indels
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DB 2; Length 453;
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Score 42;
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50.0%;
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Best Local Similarity 58.3
Matches 7; Conservative
Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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238 IDPTPEQWVK 247
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Matches 7; Conserv
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Gaps

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RESULT 14

Length 339; Indels

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MEDITME=21395368; PubMed=11815628; DOI=10.1074/jbc.M200589200; Meves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D., Makino D.L., Garratt R.C., Domont G.B., Structural and functional analyses of DM43, a snake venom metalloproteinase inhibitor from Didelphis marsupialis serum."; J. Biol. Chem. 277:13129-13137(2002).

-I. FUNCTION: Metalloproteinase inhibitor.
-I. SUBUNT: Homodimer.
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
NCBI_TaxID=9268;
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  DM43 DII
P82957;
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anopheles g
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tomato leaf
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                                                                                   26, 2005, 18:18:07; Search time 114.6 Seconds (without alignments) 67.026 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q8mis3
Q73zb2
Q7mtq9
Q8fnb0
Q8fnb0
Q53218
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Q9gz10
Q7ku30
Q24325
Q91me9
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Q8hz75
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Q8bxk6
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Q8hz73
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q8HXX5
Q8HXX5
Q8HXS3
Q73ZB2
Q77ZB2
Q7MTQ9
Q7MTQ9
Q9VQP3
Q9VQP3
Q9VQP4
Q9SZD0
Q7KU30
Q7KU30
Q7KU30
Q7KU30
Q9VUB3
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093126
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RPPL_AHSV9
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Maximum Match 100%
Listing first 45 summaries
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DM43_DIDMR
Q8HZ75
                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Match Length DB
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84
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O15070 homo sapien
Q7nfil gloeobacter
Q82tel nitrosomona
Q946h8 oryza sativ
G7vzl2 bordetella
Q7w5y0 bordetella
Q7w5y0 bordetella
Q8z76 salmonella
Q8zq06 salmonella
Q8zq06 salmonella
Q8yq45 arabidopsis
Q94457 arabidopsis
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MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;
"Isolation and partial characterization of an anti-bothropic complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria; Didelphimorphia; Didelphidae, Didelphis.
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Pred. No. 3.1e-06;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment)
Didelphis marsupialis (Southern opossum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the serum of South American Didelphidae.";
Toxicon 32:1237-1249(1994).
SEQUENCE 17 AA; 1947 MW; CB55FB40R73R2A2A CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
28-FBS-2003 (Rel. 41, Last sequence update)
26-JUL-2004 (Rel. 44, Last annotation update)
Venom metalloproteinase inhibitor DM43.
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                                                                                          QGERUS
Q7VZ12
Q7WSY0
Q7WGN4
NAGZ_SALTI
NAGZ_SALTY
Q8VM74
                                                   Q82TE1
Q946H8
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Q944S7
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Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis
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                                       SEQUENCE FROM N.A.
         NCBI_TaxID=9267;
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                                                     TISSUE=Liver;
Martinez M.E.,
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01-OCT-2002 (
01-MAR-2004 (
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Q8MIS3;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsupialis virginiana (North-American opossum).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
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                                                                               Pfam, PF00047; ig; i. -
PROSTIE, PS50835; IG LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
Metalloprotesse inhibitor; Repeat.
                                  -1- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IPR007110; Ig-like.
InterPro; IPR011015; LEM_like.
 N-glycosylated.
SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
                                                                                                                                                                                                                                                                                              Length 291;
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Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                      0; Indels
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Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY1311009; AAN06911.1; --
HSSP; O76036; 10LL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                    17A496227E69A65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AA; 15297 MW; E19D071A76AA5A7F CRC64;
                                                                                                                                                                                                               N-linked (GlcNAc. ..)
N-linked (GlcNAc. ..)
N-linked (GlcNAc. ..)
N-linked (GlcNAc. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                             Score 84; DB 1; Pred. No. 5.9e-05;
                                                                                                                                  Ig-like V-type 1.
Ig-like V-type 2.
Ig-like V-type 3.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AA
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha 1B glycoprotein DVOP51-D (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                    32390 MW;
                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.3%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                             1 LKAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPLWIKTE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 LKAMDPTPRLWIKTE 56
                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100...
Thea 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9267;
                            NOTE=Ref.1
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
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                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                 CARBOHYD
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Q8HZ75;
                                                                                                                                                             DOMAIN
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Q8HZ75
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08HZ74
1D 08HZ7
DT 01-M
DT 01-M
DT 01-M
DT 01-M
OS DIGE
OC EUKA
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Potential.
venom metalloproteinase inhibitor DM43b.
69D55F54486D35A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Didelphis marsupialis (Southern opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Didelphimorphia; Didelphidae, Didelphis.
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Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AN131001; AAN06912.1; -.
HSSP; QNVIII, 160X.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
Pfam; PF00047; ig; 1.
SWART; SM00469; IG; 1.
                                                                                                                                                                                                                         291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update
Venom metalloproteinase inhibitor DM43b precursor.
                                                                                                                                                                                                                                                          Match 89.3%; Score 75; DB 2; Local Similarity 93.3%; Pred. No. 0.0015; es 14; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 2;
Pred. No. 0.12;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL 1 23 P
CHAIN 24 314 V
SEQUENCE 314 AA; 34604 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 22, CTEMBLrel. 22, ICTEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 LKAMDTTPRLWIETE 38
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Perales J.;

SEOUENCE

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Nolson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Risen J.A., Daugherty S.C., Dodon R.J., DeBoy R.T., Paulsen I.T., Fouts D.E., Eisen J.A., Daugherty S.C., Dodon R.J., Duncan M.L., And Haft D.H., Kolonay J.F., Nolson W.C., Mason T.M., Tallon L., Gray J., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M.;

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalisters in M83.";

Tomplete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalisters in the propiet in InterPro; IPR001763; Rhodanese-like.

The Prostrick Prostrick Probanese II.

PROSITE: PSS00380; RHODANESE_1; I.

PROSITE: PSS00380; RHODANESE_3; I.
                                                                                                                                                                                                                Rhodanese-like domain protein.
OrderedLocusNames=P01887;
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                   344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13:1572-1579(2003).
EMBL; AP005221; BAC19045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 LSACDPNRPIWVESE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKAMDPTPPLWIKTE 15
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OrderedLocusNames=CB2235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 46.7 nes 7; Conservative
                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=W83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                             Q7MTQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08FNB0;
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Q8FNB0
   RESULT 8
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                      Didelphis marsupialis (Southern opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
                                                                                                                                                                                                                                                                                                                                                             "Punctional analysis of DM64, an antimyotoxic protein with immunoglobulin-like structure from Didelphis marsupialis serum."; Eur. J. Biochem. 269:6052-6062(2002).
                                                                                                                                                                                                                                                                             Rocha S.L., Lomonte B., Neves-Ferreira A.G., Trugilho M.R.,
Junqueira-De-Azevedo Id I., Ho P.L., Domont G.B., Gutierrez J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rocha S.L.G., Neves-Ferreira A.G.C., Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Ho P.L., Domont G.B., Perales J.; Submitted (FEB-2002) to the EWBL/GenBank/DDBJ databases. EMBL, AV078394 AAL82794.1; -
INERP, P24071; 1002.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
PFMMRT; SM0409; IG. 3.
PROSITE; PS50835; IG_LIKE; 4.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017233; AAS04008.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 venom myotoxin inhibitor DM64.
55975 MW; 0446529A6CBA63B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.9%; Score 52; DB 2; Length 504; 66.7%; Pred. No. 11; 3; Indels ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 227 AA; 24027 MW; 952EA4962C0EE199 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 AA
myotoxin inhibitor DM64 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                MEDLINE=22361219; PubMed=12473101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=MAP1691c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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146 LAALDPRPPLW 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                   FROM N.A.
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SEQUENCE Query Match

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Signal

05-JUL-2004

Q73ZB2

STRAIN=k10;

RESULT 7
073ZB2
AC 073Z
DT 05-J
DT 05-

Query Match

Matches

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                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                    Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
344 AA; 38572 MW; F3D938CD668BF304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                            57.1%; Score 48; DB 2; 46.7%; Pred. No. 30;
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Y4VJ_RHISN

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MEDINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F., Storeer S.E., Li P.W., Hoskins R.A., Galle R.F., Storeer S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., A storem J.R., Baradon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Ann K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Ann R.H., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Baxon A., Barman B.P., Bhandari D., Bolshakov S., Benson K.Y., Bencos P.V., Berman B.P., Brandari D., Bolshakov S., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Andrews C., Busam D.A., Bulle H. H., Cadieu E., Center A., Chandra I., Andrews B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M., A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W., Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                       AgCP7225 (Fragment).
Name=agCG51396; ORFNames=ENSANGG00000014288;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                           -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=E23; ORFNames=CG3327;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 2 C2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD8D8F CRC64;
(TrEMBLrel. 26, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0008021; C:synaptic vesicle; IEA.
GO; GO:0008215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002149; Alatroxin_recept.
InterPro; IPR008973; C2_Calb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                         preliminary data.
EMBL; AAAB01008848; EAA07048.1; -.
HSSP; P21707; 1K5W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50004; C2_DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.8%;
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PRINTS; PR00360; C2DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::|:||| |:|
294 IRALDPTNPIW 304
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Best Local Similarity
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                       01-MAR-2004
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BEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6:590-600(1996).
-!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-279 FROM N.A. MEDLINE=96389014.; PubMed=8196346; Freiberg C., Perret X., Broughton W.J., Rosenthal A.; Freiberg C., Perret X., Gruchton W.J., Rosenthal A.; Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable 'sequenase': a
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InterPro; IPR012103; Bac luciferase.
InterPro; IPR011251; Luciferase like.
PF00296; Bac luciferase; I.
Hypothetical profeln; Monooxygenase; Oxidoreductase; Plasmid.
SEQUENCE 351 AA; 39158 WW; 866BDE3B8A40C88D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid sym_pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.0%; Score 47; DB 1; Length 351; 77.8%; Pred. No. 44;
                                         Score 47; DB 2; Length 51; Pred. No. 5.9;
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                                                                                       1; Indels
759F3C5BDCCE414A CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Hypothetical 39.2 kDa protein y4vJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 AA.
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                                                                                     5; Mismatches
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                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain NGR234).
51 AA; 5686 MW;
                                         56.0%;
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                  Ouery Match
Ouery Match
Best Local Similarity 50.0%;
Best Local Similarity 50.0%;
                                                                                                                                                          Local Similarity 77.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 PrPPIWIAT 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=y4vJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium sp.
                                                                                                                                                                                                                                                                                    Y4VJ RHISN
Q53218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
SEQUENCE
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Best Loca Matches

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RESULT 11 Q70E48

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Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harian T.J., Hernandez J.R., Houck J., Harvey D., Helman T.J., Wei M.H., Ibegwan C., Howlend T.J., Wei M.H., Ibegwan C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Mcherson D., Mrhelson D., Moherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mork, Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Rainert K., Nakon K., Nisskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H., Rainer K., Sadel-Kiamos I., Simpson M., Skrong R., Suith T., Shen H., Spier E., Siden-Kiamos I., Simpson M., Skrong R., Suith T., Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Hang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Milliams S.M., Woodagfr, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., A Chibs R.A., Myers E.W., Rubin G.M., Venter J.C., The Genome sequence of Drosophila melanogaster.",

"The genome sequence of Drosophila melanogaster.",
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.

GO; GO:0000166; F:nuclectide binding; IEA.

GO; GO:0000810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=2216065; PubMed=12537568,
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirsks R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied B.J., Bartaktaroglu L., Bernan B.P. Bettencourt B.R., Celniker S.B., Gery A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AE003580; AAF51122.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3enome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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REMERICANCE FORMS AND AND AND ADDISON SOLUTION OF AND ADDISON OF PROMERCE OF C. Schorer S.E., Lip P.W., Hoskins R.A., Galle R.P., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adamstides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.P., Schitton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., M. Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeitfer B.D., R.A. Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeitfer B.D., R.A. Ballew R.M., Baul A., Baxerdale J., Andrews-Frankoch C., Baldwin D., R.A. Ballew R.M., Baul A., Baxerdale J., Andrews-Frankoch C., Baldwin D., R.A. Ballew R.M., Baul A., Baxerdale J., Andrews-Frankoch C., Baldwin D., R.A. Borkova D., Botcher A., Deuck J., Brokstein P., Brottler P., Brottler P., Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Andrews S., Delhort W. Cawley S., Dulkov D., Dew I., Dietz S.M., Andrews D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Andrews D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., R.A. Borkov B.C., Dunn P., R.A. Borkov B., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., R.A. Goor F., Gobriel M.M., Gabriellan A.E., Garriellan A.E., Garrielan A.E., Garriellan A.E., Garrielan A.E., Garrielan A.E., Garrielan A.E., Marriel B.E., Marriel B.E., Mont S.M., Moyn B., Murphy L., Marry D.M., Nelson D.L., Markel B.E., Marriel B.E., Morter B.M., Morth B.M., Marry D.M., Nelson D.L., Markel B.C., Malenn G.S., Pan S., Pollard J., Moshreil D., Weinsernbach J., R.A. Mang Z.Y., Massarman D.A., Weinsecher E., Wang A.H., Weinserder E., Spradliam S.M., Woodager, Worley Y., Sung K., Marry S.M., Woodager, Worley Y., Sung S., R. M. Woodager, Worley S., Show B.C., Schoele C., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=E23; ORFNames=CG3327;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                     Length 634;
                                                                                                                                                                                   54.8%; Score 46; DB 2; Length 634
57.1%; Pred. No. 1.2e+02;
ive 2; Mismatches 4; Indels
                                                                                                                                            634 AA; 72223 MW; A9D0900DCDB04B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         854 AA
                                                                              PROSITE, PSO0211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
InterPro; IPR003593; AAA_ATPase.
InterPro; IRR003439; ABC_transporter.
PFam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                594 LKAQNSTSPLWLNT 607
                                                                                                                                                                                                                                                                      1 LKAMDPTPPLWIKT 14
                                                                                                                                                                                                         Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000
01-OCT-2002
                                                                                                                        ATP-binding.
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                                                                                                                                         SEQUENCE
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(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    816 LKAQNSTSPLWLNT 829
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Name=E23; ORFNames=CG3327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1
nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                            01-MAR-2001
01-MAR-2004
                               01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding
                                                                                                                                                                  Name=E23;
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Matches
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Q7KU30
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                                                 MEDLINE-22456065; PubMed=12537568; MEDLINE-22456065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.W., Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AE003580; AAF51121.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                        melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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PROSITE, PS50893; ABC_TRANSPORTER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
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814 LKAQNSTSPLWLNT 827
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                            SEQUENCE FROM N.A.
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Matches
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Q9GZ10
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856 AA.

PRT;

PRELIMINARY;

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Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled to transmembrane
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Last sequence update)
Last annotation update)
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GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 00042626; F:ATP binding; IEA.
GO; GO: 0000166; F:nucleotide binding; IEA.
GO; GO: 0000166; F:nucleotide binding; IEA.
GO; GO: 0006810; P:transport; IEA.
InterPro; IPR003593; AAA ATPase.
Fam; PF00005; ABC transporter.
FAm; PF00005; ABC tran; 1.
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cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a genomics perspective.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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   coupled to transmembrane m. . .; IEA
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                                                                                                                                                                                                                           54.8%; Score 46; DB 2; Length 1017; 57.1%; Pred. No. 1.9e+02; ive 2; Mismatches 4; Indels
                                                                                                                                                                                          1017 AA; 112351 MW; D3F096E05E6EC76F CRC64;
   F:ATPase activity, coupled F:nucleotide binding; IEA
GO; GO:0042626; F:ATPase activity, couple GO; GO:0000166; F:nucleotide binding; IEA GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA, Aransporter.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR011051; RmlC_like_cupin.
ProDom; PD0000066; ABC_transporter; 1.
SMAR; PROSTIE; PS00211; AAA; 1.
PROSTIE; PS00211; ABC_TRANSPORTER 1; 1.
PROSTIE; PS50893; ABC_TRANSPORTER 2; 1.
                                                                                                                                                                                                                                                                                                                        977 LKAQNSTSPLWLNT 990
                                                                                                                                                                                                                                                                                                   1 LKAMDPTPPLWIKT 14
                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                        ATP-binding
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Matches
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Search completed: May 26, 2005, 18:43:20 Job time : 117.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

May 26, 2005, 18:17:22 ; Search time 129 Seconds (without alignments) 44.972 Million cell updates/sec

1 LKAMDPTPPLWIKTE 15 US-10-047-945-2 84 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues Searched:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqT1980s:* geneseqT0908:* geneseqD2001s:* geneseqD2001s:* geneseqD2001as:* geneseqD2003as:* A Geneseq 16Dec04:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	N-termina	N-terminu	Synthetic	Synthetic	Synthetic	N-terminu	Synthetic	Synthetic	Novel hum	Human NOV	Neisseria	Neisseria	Drosophil	TATA-bind	Drosophil	TATA-bind	Drosophil	Enterococ	Neisseria	Bovine ph	Peptide #	Human bon	Human bra	Zea mays	Zea mays
Description	Aaw11575	Aaw53841	Abb80223	Abb80225	Abb80226	Aaw53843	Abb80222	Abb80227	Abg18144	Abr 54218	Aay74721	Aay74718	Abb59797	Aar56496	Aaw06086	Aaw25029	Abb62618	Adh88053	Aay74720	Abu62528	Abb42105	Aam75798	Aam62985	Aag54516	Aag54515
ID	AAW11575	AAW53841	ABB80223	ABB80225	ABB80226	AAW53843	ABB80222	ABB80227	ABG18144	ABR54218	AAY74721	AAY74718	ABB59797	AAR56496	AAW06086	AAW25029	ABB62618	ADH88053	AAY74720	ABU62528	ABB42105	AAM75798	AAM62985	AAG54516	AAG54515
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Length DB	15	15	15	12	11	10	10	Đ	303	531	267	267	729	1189	1213	1213	1219	137	267	312	37	37	37	92	79
% Query Match	100.0	100.0	100.0	82.1	77.4	64.3	64.3	59.5	26.0	56.0	54.8	54.8	54.8	54.8	54.8	54.8	54.8	53.6	53.6	53.6	52.4	52.4	52.4	52.4	52.4
Score	84	84	84	69	65	54	54	20	47	47	46	46	46	46	46	46	46	45	45	45	44	44	44	44	44
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Aag54605 Zea mays Aag1073 Human pol Aab9318 Human pol Aab9318 Human pic Abg22890 Novel hum Adb90591 Human pit Abr47496 Breast ca Adp18673 Human pit Abr80228 Novel hum Abb80228 Syntheeic Abu23550 Protein e Abu47234 Protein e Abu47234 Protein e Abu47370 Protein e Abu47370 Protein e Abu47370 Protein e Abu47770 Protein e	Adm. 9784 tuman pro Aag27883 Arabidops Aag27882 Arabidops Aag27881 Arabidops
AAG54605 AAG54604 AAG10737 AAB93318 ABG22890 ABB90651 ABB90651 ABR47496 ABR80228 AAU323550 AAU323550 ABU23550 ABU47234 ABU45098	AAM/9/84 AAG27883 AAG27882 AAG27881
92 3 1120 4 4 1120 4 4 1120 4 4 1130 6 4 11336 8 1 1457 7 1336 8 6 1457 8 1457	522 522 687 3
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## ALIGNMENTS

Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite. N-terminal peptide from lethal toxin neutralising factor. AAW11575 standard; peptide; 15 AA. 93US-00058387. 94US-00310340. (revised)
(first entry) Didelphis virginiana. WPI; 1997-011287/01. Lipps FW, Lipps BV; (LIPP/) LIPPS B V. (LIPP/) LIPPS F W. 22-SEP-1994; 10-MAY-1993; 25-MAR-2003 20-MAR-1997 US5576297-A. 19-NOV-1996. AAW11575; AAW11575 

Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.

Claim 7; Col 9; 9pp; English.

The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity to the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 15 AA;

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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                    ABB80223 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-2003; 2003WO-US001044.
                                                                                                        (first entry)
                                                                                                                                           Synthetic LTNF, LT-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                        WO2003060471-A2.
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                                                                                                        06-NOV-2003
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                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                     ABB80223;
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RESULT 3
                    ABB80223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) molety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Elapidee, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                     LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 84; DB 2; Length 15; 100.0%; Pred. No. 2.1e-06; ive 0; Mismatches 0; Indels
                  Length 15;
                                                   Indels
              100.0%; Score 84; DB 2; L
100.0%; Pred. No. 2.1e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                               AAW53841 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00657163
                                                                                      1 LKAMDPTPPLWIKTE 15
                                                                                                                   1 LKAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                      N-terminus of opossum LTNF.
                                                                                                                                                                                                                                                                                   (first entry)
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipps FW, Lipps BV;
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К.
                                 Local Similarity
les 15; Conserv
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(LIPP/) LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USS744449-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1993;
22-SEP-1994;
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                                                                                                                                                                                                                                                AAW53841;
                  Query Match
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                                                 Matches
                                                                                                                                                                                           AAW53841
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The sequences given in ABBB0222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (19E), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum ISE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, dalisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva canlection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from requires a more complicated sandwich type ELISA
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100.0%; Pred. No. 2.1e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 3; 24pp; English.
14-JAN-2002; 2002US-00047945.
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ses 15; Conservative
                                                                                                                                                                                     Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                           WPI; 2003-636703/60.
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RESULT 4 ABB80225

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Gaps

; 0

1 LKAMDPTPPLWIKTE 15 

δ

15; Conservative

Local Similarity

Best Loca Matches

al toxin neutralising factor; LTNF; serum protein; immunoglobulin B; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; es' disease; Addison's disease; Hodgkin's disease; depression;

Synthetic LTNF, LT-11.

Lethal

14-JAN-2003; 2003WO-US001044. 14-JAN-2002; 2002US-00047945

WO2003060471-A2.

24-JUL-2003.

**Baliva**; ELISA

Graves'

Synthetic.

Lipps BV, Lipps FW; WPI; 2003-636703/60.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva confliction is relatively non-invasive when compared to blood collection of the protein is relatively non-invasive when compared to blood collection of the protein had been deminated immediately, whereas blood requires
                                                                                                   Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 4; 24pp; English.
ABB80225 standard; peptide; 12
                                                                                                                                                                                                                                                                              14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                        14-JAN-2002; 2002US-00047945.
                                                 (first entry)
                                                                             Synthetic LTNF, LT-12
                                                                                                                                                                                                                                                                                                                                                                           Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-636703/60.
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                                                                                                                                                                                                                          WO2003060471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
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                                                   06-NOV-2003
                                                                                                                                                                                                                                                    24-JUL-2003
                                                                                                                                                                                                 Synthetic
                        ABB80225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patient.
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e.9

Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a

Claim 7; Page 4; 24pp; English.

patient.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTRF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (ISE), nerve growth factor (NGF), insulin, myoglobin and/or adenosinse (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum ISE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifued immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.4%; Score 65; DB 7; Length 11; 100.0%; Pred. No. 0.0016; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                              assayed by a simple ELISA test
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
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Gaps ö

82.1%; Score 69; DB 7; Length 12; 100.0%; Pred. No. 0.0004; ive 0; Mismatches 0; Indels

12; Conservative

Matches

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Local Similarity

Query Match

ABB80226 standard; peptide; 11 AA

RESULT 5
ABB80226
ID ABB8
XX
AC ABB8

ABB80226;

US5744449-A 28-APR-1998

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (IgE), insive growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (BLISA) on a saliva canlescent in elevant that is specific for the protein. Saliva can be centrifuged immediately, whereas blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple BLISA test, whereas an assay of proteins from serum requires a more complicated sandwich type BLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                               Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.078; 1.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80227 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 3; 24pp; English.
                                                                                                                                14-JAN-2003; 2003WO-US001044
                                                                                                                                                                                14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic LINF, LT-9.
                                                                                                                                                                                                                                                                                                              Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LKAMDPTPPL
                                                                                                                                                                                                                              (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                          WO2003060471-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                saliva; ELISA.
                                                                             24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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  %XXCCCCCCCCCCCCX8X44444X4X4X4X4X4X4X4XAXAXAXAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemornhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomention from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                             LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Siongram, 8 syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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64.3%; Score 54; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80222 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Col 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                    96US-00657163
                                                                                                                                                                                                                                                                                                                                                                                       93US-00058387
94US-00310340
                                                                                                                                histamine reaction treatment
N-terminus of opossum LTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKAMDPTPPL 10
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                                                                                                                                                                              Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-271108/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                      03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1994;
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Gaps

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WO2003060471-A2

Synthetic.

saliva; ELISA

ABB80222;

RESULT 7

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Synthetic

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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR54218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR54218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                        The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogran's syndrome, Relier's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva cample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection of for a serum. Saliva can be centrifugation to separate serum. Saliva proteins from be assayed by a simple BISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.5%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #18135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG18144 standard; protein; 303 AA.
                                                                                                                                                                                                       Claim 7; Page 4; 24pp; English.
                     14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                          14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LKAMDPTPP 9
                                                                                                   Lipps BV, Lipps FW;
                                                                                                                          WPI; 2003-636703/60
                                                                 (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
24 -JUL-2003.
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                                                                                                                                                                                 patient.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromesome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cupplypeptide and polynucleotide sequences have applications in disorders collypeptide and polynucleotide sequences have applications in collypeptide and polynucleotide sequences have applications of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and canino acid sequences. ABGOOID-ABGI30377 represent novel human dispnostic patent did not appear in the printed specification, but was obtained in the with printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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Pred. No. 35;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 48503; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV21a protein SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR54218 standard; protein; 531 AA.
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.0%;
Best Local Similarity 42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 EASDPVPPYWVRLQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolic syndrome X.
                                                                                              WPI; 2001-639362/73.
N-PSDB; AAS82331.
Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity.
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The present invention describes isolated human NOVX proteins, where X is

1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
ABR54167 to ABR54276. NOVX sequences have antiatheroscalerotic, cardiant,
hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
antidiabetic, metabolic, immunomodulator, neuroprotective, noctropic,
antidiate, metabolic, immunomodulator, neuroprotective, noctropic,
antiparkinsonian and antilipaemic activities, and can be used in gene
therapy. NOVX proteins are useful for treating or preventing a pathology
associated with a NOVX protein in humans and for treating a syndrome
associated with the human disease. NOVX mucleic acids, proteins and
antibodies can be used in the treatment and diagnosis of cardiomyopathy,
throaccalcrosis, hypertension, congenital heart defects, acids, metabolic
alve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
disorders, neoplasm, lymphom, uterus cancer, fertility, haemophilia,
hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
disease, AlDS, bronchial asthma, Crohn's disease, multiple sclerosis,
infectious disease, anorexia, cancer-associated cachexia, cancer,
hematopoletic disorders, dysliddaemias, and metabolic syndrome X.
ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human proteins and nucleic acid encoding the proteins, useful for diagnosis, treatment and prevention of disorders involving the human protein or nucleic acid e.g. cardiac and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
Crabtree J, Dipippo VA, Edinger SR, Elsen AJ, Ellerman KJ,
Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
Malyankar UM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M;
Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
Spaderna SK, Spytek KA, Taupler RJ, Twomlow N, Vernet CAM, Voss EZ
Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 173; 460pp; English.
                                                                                                                                                                                                                                                                                                                                                         25-SEP-2001; 2001US-0324969P.
25-SEP-2001; 2001US-03259JP.
26-SEP-2001; 2001US-032499P.
14-DEC-2001; 2001US-0341144P.
26-FEB-2002; 2002US-035959P.
03-MAX-2002; 2002US-0373989P.
                                                                                                                                                                                                          2001US-0322636P.
2001US-0322816P.
2001US-0322817P.
2001US-0323817P.
2001US-0323519P.
2001US-0323631P.
                                                                                                                                              2001US-0318120P.
2001US-0318184P.
2001US-0318430P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-2002; 2002US-0383863P.
02-JUL-2002; 2002US-039332P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002US-0381483P
                                                                                                       09-SEP-2002; 2002WO-US028538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-313241/30.
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                   WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                         20-SEP-2001;
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                                                             20-MAR-2003
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY55941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be
              ABRS4277 represents a human trypsinogen protein given in comparison with
the human NOV35b protein in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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Scalato E, Scarselli M;
                                                                                                                            Gaps
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sequences, which are used in examples from the present invention.
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                                                                                           6; Length 531;
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Ratti G,
                                                                                          Score 47; DB
Pred. No. 64;
                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                    AAY74721 standard; protein; 267 AA.
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, Pizza M, Rappuoli R,
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98US-009889P.
98US-0098994P.
98US-0099062P.
98US-0103749P.
                                                                                        56.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; gene therapy.
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                                                                                                                          8; Conservative
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                                                                                                                                                          4 MDPTPPLWIKTE 15
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Venter JC;
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                                                                                                            Best Local Similarity
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                                                               Sequence 531 AA;
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Tettelin H,
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09-0CT-1998
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Chaudhuri A;
Ellerman K;
o X, Gusev VY, Ji W;
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AAR56496 standard; protein; 1189 AA.
 Sequence 267 AA;
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                                                                                                                                                                                                                                      pharmaceutical
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                                                                                                                                                                                                                          Drosophila;
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                                                                                                                                                             ABB59797;
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AAR56496
ID AAR56
                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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Scalato E, Scarselli M;
                                                               Gaps
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                               DB 3; Length 267;
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Ratti G,
                                                               2; Mismatches
                                           Score 46;
Pred. No.
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Pizza M, Rappuoli R,
Venter JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 553; 1453pp; English.
used in gene therapy protocols
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98US-0098994P.
98US-0099062P.
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98US-0103796P.
                                          54.8%;
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                                                                                                                                                                                                                                                                    antibacterial; gene therapy.
                                                                                                                                                                                                      (first entry)
                                        Ouery Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                    3 AMDPTPPLWIKT 14
                                                                                                        AKHPTPPTWLQT 20
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N-PSDB; AAZ53480.
                       Sequence 267 AA;
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09-OCT-1998;
25-FEB-1999;
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Petersen J,
Tettelin H,
                                                                                                                                                                                                      21-MAR-2000
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02-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176-ABL30511), expressed DNA aequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
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  Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 6183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 4; I
Pred. No. 1.3e+02;
2; Mismatches 4;
  DB 3;
  Score 46; DB 3
Pred. No. 45;
2; Mismatches
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11-JUL-2000; 2000US-00614150.
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     54.88;
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689 LKAQNSTSPLWLNT 702
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                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
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Best Local Similarity 57.1.
Rest Local 8; Conservative
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Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                   AKHPTPPTWLQT 20
                                                                                                    3 AMDPTPPLWIKT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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TFIID; fraction;

Ruppert S, Weinzierl ROJ, Tjian R;

Tanese N,

Dynlacht BD;

Hoey T,

94US-00188582. 93US-00013412.

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Screen for cpds, that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved in disease.
            Drosophila TATA-binding protein associated factor dTAFII150 protein.
                                   Drosophila, TATA-binding protein, TBP associated factor, 'RNA polymerase II, transcription, messenger RNA, nuclear holoenzyme, lambda-gtll; expression library.
                                                                                                                                                                                                                                                                                                                                                                     Example; Col 123-132; 86pp; English
                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                   WPI; 1996-333245/33.
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                                                                                                                                                             28-JAN-1994;
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                                                                                                            US5534410-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The TATA-binding protein associated factor hTAPISO (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific blochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating gene expression associated with human pathology. (Updated on 25-MAR-2003 to correct PN
                                                                                               protein associated factor; dTAFISO; screening; diagnostic; gene transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATA-binding protein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies, useful in screening, diagnostics and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                     Tanese N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.8%; Score 46; DB 2; Length 1189; Best Local Similarity 53.3%; Pred. No. 2.1e+02; Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Comai L, Dynlact BD, Hoey T, Ruppert S, Weinzierl ROJ;
                                                                      TATA-binding protein-associated factor dTAFISO.
                                                                                                                                                                                                   /note= "Arg, Pro or His"
1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 156; 180pp; English
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                  'note= "Val or Leu"
                                                                                                                                                                                                                                 'note= "STOP"
                                                                                                                                                                                                                                                         /note= "STOP"
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                                                                                                                                                                                                                                                                                                                                                       93US-00013412,
93US-00087119.
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-264019/32.
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                                                                                                                                                           Key
Misc-difference
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                                                                                                                                                                                              Misc-difference
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                                  25-MAR-2003
23-MAR-1995
                                                                                             TATA-binding
                                                                                                                                                                                                                                                                                                                                                       28-JAN-1993;
30-JUN-1993;
                                                                                                            therapeutic;
                                                                                                                                                                                                                                                                                                         04-AUG-1994.
                                                                                                                                     Drosophila
            AAR56496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Wang E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          field.)
8XCCCCCCCXXX441XX88X15X3X4X4X4X4X11111111XXXX4X8X6X1512X4X
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This is the amino acid sequence of the Drosophila TATA-binding protein (TBP) associated factor (TAF) designated TAFII60. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 60 kD by SDS-PAGE. The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIID, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID expression allowed cloning of the corresp. genes from lambda-gtil erraction libraries. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; I
Pred. No. 2.2e+02;
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nes 8; Conservative
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Gaps

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AAW06086 standard; protein; 1213 AA.

RESULT 15 AAW06086 (first entry)

(revised)

25-MAR-2003 27-JAN-1997

AAW06086;

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May 26, 2005, 18:43:39 ; Search time 98.4 Seconds (without alignments) 52.587 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_PUBGOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1462099 seqs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPPLWIKTE 15
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 4, Appl1	Sequence 5, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 104, App	Sequence 278038,	Sequence 200494,	Sequence 173148,	•	Sequence 45321, A	Sequence 229035,	Sequence 255201,
	QI	US-10-047-945-2	US-10-047-945-4	US-10-047-945-5	US-10-047-945-1	US-10-047-945-6	US-10-236-417-104	US-10-424-599-278038	US-10-437-963-200494	US-10-424-599-173148	US-09-885-303A-16	US-09-864-761-45321	US-10-424-599-229035	US-10-424-599-255201
	80	14	14	14	14	14	15	15	16	15	10	0	15	15
	Match Length DB ID	15	12	11	10	6	531	85	384	41	312	37	70	106
* Ouerv	Match	100.0	82.1	77.4	64.3	59.5	56.0	54.8	54.8	53.6	53.6	52.4	52.4	52.4
	Score	84	69	65	54	20	47	46	46	45	45	44	44	44
Result	No.	н	7	6	4	2	9	7	80	6	10	11	12	13

SERUM

OTHER INFORMATION: SYNTHESIZED, ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2

Query Match 100.0%; Score 84; DB 14; Length 15; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 15; Conservative 0; Mismatches 0; Indels

1 LKAMDPTPPLWIKTE 15 

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Gaps

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FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Corresponds to fragment 1-12 of 2 above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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   Sequence 4, Application US/10047945
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE:
; RIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10047945
Publication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
FILE REPERENCE: FWLPATION (IGE) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE: 2002-01-14
PRIOR FILING DATE:
PRIOR FILING DATE:
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100.0%; Pred. No. 0.0053;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.1%; Score 69; DB 14;
100.0%; Pred. No. 0.0015;
ive 0; Mismatches 0
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 5
ERNOTH: 11
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US-10-047-945-1
; Sequence 1, Application US/10047945
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity
Matches 11; Conserva
US-10-047-945-4
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US-10-047-945-5
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                     APPLICANT: LIPPS, FREDERICK W.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1981) IMPLICATED DISORDERS

FILE REFERENCE: FWLPATOISUS

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT PILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO

LENGTH: 10

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10047945
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
    APPLICANT: LIPPS, BINIE V.
    APPLICANT: LIPPS, REBERICK W.
    TITLE OF INVENTION: (198) IMPLICATED DISORDERS
    TITLE OF INVENTION: (198) IMPLICATED DISORDERS
    FILE REFERENCE: FWLPATO15US
    CURRENT APPLICATION NUMBER: US/10/047,945
    CURRENT FILING DATE: 2002-01-14
    PRIOR APPLICATION NUMBER:
    PRIOR APPLICATION NUMBER:
    NUMBER OF SEQ ID NOS: 7
    SOPTWARE: WORDPERFECT 5.1 FOR WINDOWS
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Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.5%; Scc. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.3%; Score 54; DB 100.0%; Pred. No. 0.2 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
COTHER INFORMATION: SYNTHESIZED.
COTHER INFORMATION: US 5,576,297.
US-10-047-945-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Synthetic.
US-10-047-945-6
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US20030157555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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SERUN

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Sequence 200494, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Application, Mu, Wei
    APPLICANT: Barbaruk, Brad
    APPLICANT: Barbaruk, Brad
    APPLICANT: Butharov, Andrey A.
    APPLICANT: Butharov, Andrey A.
    APPLICANT: Butharov, Andrey A.
    APPLICANT: Barbaruk, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21(53221)B
    CURRENT APPLICATION NUMBER: US/10/437,963
    CURRENT PLING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
    SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Las Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: PLANTS: 2016/3223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 173148
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 16; Length 384;
Pred. No. 1e+02;
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US-10-424-599-173148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION; Clone ID: PAT_MRT4530_95958C.1.pep
US-10-437-963-200494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || |||| : |
14 DPIPPLWAQPE
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ORGANISM: Glycine max
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US-09-885-303A-16
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Publication Wo. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cavo Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 278038
LENGTH: 85
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### PEDICANT: Agee et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPRENENCE: 21402-442C

CURRENT APPLICATION NUMBER: US/10/236,417

CURRENT PILING DATE: 2001-09-06

PRIOR PEDICATION NUMBER: US60/318,120

PRIOR PEDICATION NUMBER: US60/318,430

PRIOR PEDICATION NUMBER: US60/322,781

PRIOR PEDICATION NUMBER: US60/322,781

PRIOR PEDICATION NUMBER: US60/322,781

PRIOR PEDICATION NUMBER: US60/326,633

PRIOR PELING DATE: 2001-09-07

PRIOR PEDICATION NUMBER: US60/36,412

PRIOR PELING DATE: 2002-03-05

PRIOR PELING DATE: 2001-09-07

PRIOR PELING DATE: 2001-09-17

PRIOR PELING DATE: 2001-09-19

PRIOR PELING DATE: 2001-09-19
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US-10-424-599-278038
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Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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70 MDTSPPLWTLTE 81
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ORGANISM: Homo sapiens
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45 TPPLWVKIE 53
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Gaps

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Gaps

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Sequence 229035, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongweil
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 285684
LENGTH: 70
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
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OTHER INFORMATION: MAP TO AL133458.11
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
OTHER INFORMATION: SWISSPROT HIT: 053951, EVALUE 6.40e+00
OTHER INFORMATION: EST_HUMAN HIT: A19864481.1, EVALUE 6.00e-16
US-09-864-761-45321
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   PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ.ID NO 45321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB pred. No. 22; 4; Mismatches
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Best Local Similarity 46.2
Matches 6; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Publication No. US20030032078A1
GENERAL INFORMATION:
APPLICANT: TRAVIS, GABRIEL H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF MACULAR
TITLE OF INVENTION: AND RETINAL DEGENERATIONS
FILE REFERENCE: UTSD:758US
CURRENT PELLING NUMBER: US/09/885,303A
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 60/263,837
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
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Pred. No. 1.2e+02;
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CURRENT APPLICATION NUMBER: US/09/664,761

CURRENT PAPLICATION NUMBER: US/09/664,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELLING DATE: 2000-02-04

PRIOR PLLING DATE: 2000-02-04

PRIOR PLLING DATE: 2000-06-26

PRIOR PLLING DATE: 2000-06-26

PRIOR PLLING DATE: 2000-06-06

PRIOR PLLING DATE: 2000-09-07

PRIOR PPLICATION NUMBER: US 60/236,356

PRIOR PELLING DATE: 2000-10-04

PRIOR PELLING DATE: 2000-10-04

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30
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Best Local Similarity 57.1%;
Matches 8; Conservative
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268 LKAMDPSGSLYVRT 281
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; ORGANISM: Bos taurus
US-09-885-303A-16
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Search completed: May 26, 2005, 19:17:13
Job time : 138.4 secs
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US-10-424-599-205702
is Gequence 205702, Application US/10424599
is Publication No. US20040031072A1
is GENERAL INFORMATION:
is APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
is TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
is TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
is TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
is TITLE OF SEQ ID NOS: 285684
is CURRENT APPLICATION NUMBER: US/10/424,599
is CURRENT PLING DATE: 2003-04-28
is NUMBER OF SEQ ID NOS: 285684
is SEQ ID NO 205702
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151167, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With:
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILIE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 151167
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                                                                                                                                                                                                              Score 44; DB 15; Length 106;
Pred. No. 60;
1; Mismatches 0; Indels
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US-10-424-599-151167
                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
US-10-424-599-255201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 EEQ ID NO 255201 LENGTH: 106
                                                                                                                                                                                                                   52.4%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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ORGANISM: Glycine max
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                                                                                      TYPE: PRT
ORGANISM: Glycine max
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LOCATION: (1)..(144)
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Pred. No. 80;
1; Mismatches 0; Indels
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
CHER INFORMATION: Clone ID: PAT_MRT3847_27777C.1.pep
US-10-44-599-205702
                                                                                                   Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Sequence 1, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 13316, A
Sequence 1337, Ap
Sequence 43223, A
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1353, Ap
Sequence 1555, A
Sequence 44479, A
Sequence 44501, A
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15, Appl
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18, Appl
45215, A
1166, Ap
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                                                                                                                                May 26, 2005, 18:29:58 ; Search time 34.2 Seconds (without alignments) 32.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1
Sequence 1
Sequence 8
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-396A-18
US-09-270-767-45215
US-09-710-279-1166
US-09-248-796A-20923
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US-08-657-163A-1

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US-09-134-000C-5938

US-09-134-000C-5938

US-09-732-210-1367

US-09-732-210-1367

US-09-732-210-1367

US-09-732-210-1353

US-09-770-767-4255

US-09-270-767-4255

US-09-270-767-4255

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US-09-270-767-4265

US-09-270-767-4265
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB E
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                                                                                                                                     Run on:
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US-08-310-340A-1

Sequence 1, Application US/08310340A

Sequence 1, Application US/08310340A

Sequence 1, Application US/08310340A

SEQUENCE 1, Application US/08310340A

GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 1
CORRESPONDENCES: 1
CORPUTER: BINIE V. LIPPS

STREET: 45.09 MINOSA DR.

COUNTRY: USA

ZIP: 77401

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: TEM COMPATIBLE

COMPUTER: TEM COMPATIBLE

COMPUTER: TEM COMPATIBLE

COMPUTER: TEM COMPATIBLE

COMPUTER: NS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,340A

FILING DATE: 10 MAY 1993

ATTORNEY/ACENT INFORMATION:

NAME: NAME: NAMEDED.

NAME: NAMEDED.

NAME: NAMEDED.

NAME: NAMEDED.

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PROPERTY OF THE NAMEDED.

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Sequence 4103, Ap Sequence 104, App Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 2, Appl Sequence 7219, Ap Sequence 7219, Ap Sequence 56512, A Sequence 21938, A Sequence 21938, A
                                                                                                                                                                                                                                                                                                               Sequence 21938, A
Sequence 6054, Ap
Sequence 42, Appl
Sequence 14895, A
                                         US-08-463-0818-134
US-08-461-3794-14
US-08-462-3908-14
US-08-462-3908-14
US-08-465-685-14
US-08-465-64-1
US-09-949-016-7610
US-09-949-016-767-41296
US-09-252-991A-21938
US-09-252-991A-21938
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US-09-252-991A-21938
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US-09-902-540-14895
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ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRINIANA
STRAIN: WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: PROTEIN IN SEQ ID HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEPAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: SINGLE TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15
TYPE: AMINO ACID
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SEQUENCE CHARACTERISTICS
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Patent No. 574449

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STREET: TEXAS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND NOTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FABDABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 13.5" FLOPPY DISK, 1.44 MB
COMPUTER: 13.5" FLOPPY DISK, 1.44 MB
COMPUTER: 13.6" FLOPPY DISK, 1.44 MB
COMPUTER: 13.6" FLOPPY DISK, 1.44 MB
COMPUTER: 3.5" FLOPPY DISK, 1.44 MB
SOPTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FLIING DATE: 22 SEPTEMBER 1994
CLASSIPTCATION 1514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAMME: JOHN R. CASPERSON
REGISTRATION NUMBER: 26,198
                                    HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
CLIDRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
FELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
  TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPLWIKTE 15
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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US-08-310-340A-1
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CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08657163A
Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: BINIE V. LIPPS
GROEDER: ALLEY V. LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 84; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
                                                                                                                                                                    OPOSSUM SERA: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
                      STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO:
HYPOTHETICAL: NO
                                                                                                                ANTI-SENSE: NO
FRACHENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SE
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILLING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                        TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BINIE V. LIPPS STREET: 4509 MIMOSA DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPLWIKTE 15
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AMINO ACID
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                    HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-8 NOV 1991
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                    ORGANELLE
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, MOLECULE TYPE: protein US-08-646-715-20
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APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hosy, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinsierl, Kobert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.3%; Score 54; DB 1; Length 10; 100.0%; Pred. No. 0.031; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-57650-2/AJT/RAO
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REPERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECPHONE: 713-482-2961
TELEFPHONE: 713-663-7290
                                                                                                                                                                                                                   SEQUENCE CALL TO LENGTH: 10
TYPE: AMINO ACID
STRANDENESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08188582 Patent No. 5534410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ogman, Richard A
REGISTRATION NUMBER: 36,627
REPRENCE/DOCKET NUMBER: A-57
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tjian, Robert
Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                US-08-657-163A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-188-582-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Slegfried
APPLICANT: Tanee, Naoko
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
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Query Match 54.8%; Score 46; DB 1; Length 1213; Best Local Similarity 53.3%; Pred. No. 74; Matches 8; Conservative 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUUNTRY: USA

ZIP: 94111-4187

ZIP: 94111-4187

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,715

FILING DATE: 09-MAY-1996

CLASSIPICATION: 435

PROCESSIPICATION: 435

PROCESSIPICATION NUMBER: US/08/188,582

PILING DATE: 28-JAN-1994

ATRONEY/AGENT INFORMATION:

NAME: OGMAN, RACHARD 43

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 36,627

RELEPRAK: (415) 781-1989

TELEFRAK: (415) 781-1989

TELEFRAK: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
74;
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                                                                                                                                                                                                                                                                     Sequence 20, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
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620 LSAMDDSPVLWIRLD 634
                                                                                                1 LKAMDPTPPLWIKTE 15
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tjian, Robert
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Gaps

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US-09-270-767-4323

Sequence 43223, Application US/09270767

Sequence 43223, Application US/09270767

Sequence 43223, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 43223

LENGTH: 253
                 TITLE OF INVENTION: ALLI-fungal Proteins and Methods for Their Use FILE REFERENCE: 38-21(15.056)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR PLILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
LENGTH: 151
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Richard H.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Marlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Broduction
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                             48.8%; Score 41; DB 4; Length 151; 75.0%; Pred. No. 50; 1; Indels ive 1; Mismatches 1; Indels
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STREET: 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/09036987A; Patent No. 6143526; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ADDRESSEE: Dow Agros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TPPLWIKT 14
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Best Local Similarity
Matches 6; Conserv
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US-09-732-210-1367
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US-09-036-987A-5
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                                                                                             Sequence 5938, Application US/09134000C

Patent No. 6617156

Patent No. 6617156

Fatent No. 6617156

Fatent No. 6617156

Fatent No. 6617156

Fatent No. 6617156

FATILE OF INVENTION: UNCLETC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNMERS. US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PATENT PATENT NOS: 6812

SOFTWARE PATENT NOS: 6812

SOFTWARE PATENT NOS: 6812

SEQ ID NO 5938

LENGTH. 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-902-540-13316

1 Sequence 13316, Application US/09902540

2 Sequence 13316, Application US/09902540

3 Patent No. 6833447

3 GENERAL INFORMATION:

3 APPLICANT: Goldman, Barry S.

4 APPLICANT: Miegand, Reger C.

5 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof.

5 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof.

6 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof.

7 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences.

8 FILE REFERENCE: 38-10(15849)B

9 CURRENT FILING DATE: 2001-07-10

9 PRIOR PRILING DATE: 2001-07-10

9 PRIOR SEQ ID NOS: 16825

9 SEQ ID NO 13316

1 LENGTH: 397
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Pred. No. 11;
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Pred. No. 68;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%;
620 LSAMDDSPVLWIRLD 634
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Best Local Similarity 66.7%;
Matches 6; Conservative
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; ORGANISM: Myxococcus xanthus
US-09-902-540-13316
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85 NPTPPLWV 92
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                                                                  RESULT 6
US-09-134-000C-5938
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Length 253; Indels

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Sequence 5, Application US/09603207B Patent No. 6521406
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21 TPPSWLKT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV.
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DAFE: 1999-08-09
BARLIER APPLICATION NUMBER: US 09/36987
BARLIER APPLICATION NUMBER: US 09/36987
BARLIER PATENCE DATE: 1998-03-09
SOFTHARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%; Score 41; DB 3; Length 4928; 50.0%; Pred. No. 1.9e+03;
                                                      COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURAGEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,479
REGISTRATION NUMBER: 28,479
REGISTRATION INFORMATION:
TELEPHONE: (317)337-4847
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.96
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Saccharopolyspora spinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09370700 Patent No. 6274350
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2850 LRAADVSAPLWLAT 2863
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserva
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RESULT 12

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Patent No. 657361

GENERAL INFORMATION:

APPLICANT: Bunkers, Greg J.

APPLICANT: Mittanck, Cindy A.

APPLICANT: My Younie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use FILE REFREBRUCE: 38-21(15036)B

CURRENT PRICATION NUMBER: US/09/732,210

CURRENT FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Baltz, Richard H

APPLICANT: Broughton, Mary C

APPLICANT: Crawford, Kathryn P

APPLICANT: Treadway, Patti J

APPLICANT: Turner, Jan R

APPLICANT: Turner, Jan R

APPLICANT: Turner, Jan R

APPLICANT: Turner, Jan R

CURRENT FILING BATE: 2000-06-23

CURRENT PILING DATE: 1998-03-09

MUNDER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 4928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
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; Sequence 57545, Application US/09270767
: Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-603-207-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.6%;
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US-09-732-210-1353
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Best Local Similarity 75.0
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RESULT 15
US-09-270-767-42501
US-09-270-767-42501

Sequence 42501, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
PAPLICANT: Homburger et al.
TILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
TILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 42501

LENGTH: 303

TYPE: PRT

ORGANISM: Drosophila melanogaster
US-09-270-767-42501
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 57545
LENGTH: 198
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47.6%; Score 40; DB 4; Length 303;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                            Score 40; DB 4; Length 198;
Pred. No. 95;
3; Mismatches 2; Indels
                                                                                                                                                                                         TYPE: PRT CREANISM: Drosophila melanogaster FEATURE: FEATURE: POTHER INFORMATION: Xaa means any amino acid US-09-270-767-57545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 26, 2005, 19:08:38 Job time : 35.4 secs
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Best Local Similarity 54.5
Matches 6; Conservative
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95 LQPTPELWTQT 105
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70 IKAVSPSPNLW 80
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2005, 18:26:23 ; Search time 7.9 Seconds (without alignments) 60.897 Million cell updates/sec Run on:

US-10-047-945-3 24 Title: Perfect score:

1 LKAMD 5 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	OI	Description
1	24	100.0	96	2	AI1916	hypothetical prote
7	24	100.0	144	~	B83114	~
e	24	100.0	145	7	D83424	hypothetical prote
4	24	100.0	178	~	A38593	
'n	24	100.0	185	Н	LZWSG	lysozyme (EC 3.2.1
9	24	100.0	202	~	AE3377	queuine tRNA-ribos
7	24	100.0	210	~	T14734	NSS protein - sorg
89	24	100.0	213	~	F69838	opine aminotransfe
σ	24	100.0	237	7	A42013	alpha-1-B-glycopro
10	24	100.0	253	~	JC5709	maleate isomerase
11	24	100.0	256	N	C71546	probable glucose-6
12	24	100.0	270	М	CCECID	cell division inhi
13	24	100.0	270	N	AH0724	
14	24	100.0	270	~	F85695	cell division inhi
15	24	100.0	270	N	E90837	cell division inhi
16	24	100.0	272	~	E95144	Cof family protein
17	24	100.0	272	~	C98012	conserved hypothet
18	. 24	100.0	279	~	S58402	synaptotagmin V -
19	24	100.0	304	~	I39049	alpha (1,3) fucosy
20		100.0	305	N	T09370	shikimate kinase h
21	24	100.0	306	~	B54717	palmitoyl-protein
22	24	100.0	359	~	A45156	alpha-(1,3)-fucosy
23	24	100.0	364	N	I39048	alpha (1,3) fucosy
24		100.0	364	~	S43117	transposase - Lept
25		100.0	7	N	H87450	ě
26	24	100.0	377	N	AD3363	queuine tRNA-ribos
27	24	100.0	379	Н	DWDXBF	2-hydroxyglutaryl-
28	24	100.0	381	~	B69722	queuine tRNA-ribos
53	24	100.0	385	~	AD0528	conserved hypothet

hypothetical prote 3-ketoacyl-coa thi	probable nonspecif hypothetical prote	cellutagmin II syt arylsulfatase regu	phow family protei	transcription fact ATPase [imported]	ATPase - Chlamydop	transcription fact transcription fact	cellobiose phospho	phosphomannomutase	moaA/NirJ family F	hypothetical prote
F90649 F75047	E71113 F85500	S58400 D69525	F81552	S34449 C86504	B72118	A31752 S42111	C69785	G64349	D97243	T17332
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385 388	389 391	403	424	428	428	437	442	449	461	464
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2 4 4 4	24	24 24	24	2 4	24	2 4 4 4	24	24	74	24
30 31	33 33	34 35	36	38	39	40 41	42	43	44	45

## ALIGNMENTS

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H	1916
9	⇉
3	5

hypothetical protein as10884 [imported] - Nostoc sp. (strain PCC 7120)

CiSpecies: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: A11916

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A,Accession: AI1916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 «KUR>
A;Cross-references: UNIPROT:QBYYGG; GB:BA000019; PIDN:BAB72841.1; PID:g17130229; GSPDB:GA;Experimental source: strain PCC 7120

C, Genetics:

A;Gene: as10884 C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology

барв ö Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels

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1 LKAMD 5 ઠે

23 LKAMD 27 g

50S ribosomal protein L15 PA4244 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa C;Date: 1.5-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: B83114 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .: Lory, S.; Olson, M.V.

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043

A,Accession: B83114
A,SCatus: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Rocidues: 1-144 CATO>
A,CCOSS-references: UNIPROT:Q9HWF4; GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG0763
A,Experimental source: strain PAO1

A;Gene: rplo; PA4244 C;Superfamily: Escherichia coli ribosomal protein L15

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A; Molecule type: protein
A; Mesidues: 1-185 < 65IN-
A; Residues: 1-185 < 65IN-
A; Cross-references: UNIPROT: P00717
R; Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
R; Jahnen, W.; Ward, Commun. 166, 139-145, 1990
A; Title: Internal amino acid sequencing of proceedins by in situ cyanogen bromide cleavage
A; Reference number: A90157; MUID: 90147691; PMID: 2302197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Description: catalyzes hydrolysis of the beta-1,4-glycosidic bond between N-acetylmura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: lysozyme g
Kewywords: bacteriolytic enzyme; egg white; glycosidase; hydrolase; polysaccharide degr
F;4-60,18-29/Disulfide bonds: #status predicted
F;73,86/Active site: Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                queuine tRNA-ribosyltransferase (EC 2.4.2.29) [imported] - Brucella melitensis (strain 1º
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessi Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q8YH02; GB:AE008917; PIDN:AAL52184.1; PID:g17982964; GSPDB:C
                      Risimpson, R.J.; Begg, G.S.; Dorow, D.S.; Morgan, F.J.
Biochemistry 19, 1814-1819, 1980
A; Title: Complete amino acid sequence of the goose-type lysozyme from the egg white of
A; Reference number: A00872; MUID:80198318; PMID:7378374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 'X',47-59'X',61-68;95-99,'X',101-106,'X',108,'X',110-111 <JA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 24; DB 1; Length 185; 100.0%; Pred. No. 60; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 24; DB
100.0%; Pred. No. 66;
ive 0; Mismatches
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Matches 5; Conservative
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C; Accession: A00872; B34047
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Matches 5; Conserv
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cipecies: Peeudomonas aeruginosa
Cipacies: Peeudomonas aeruginosa
Cipacies: Peeudomonas aeruginosa
Cipacies: Desdep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cipacies: D83424
A. Stover, C. K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradaman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jacust 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon. A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon. A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon. A.Title: D83424
A.Stetun: preliminary
A.Stetun: preliminary
A.Stetun: D83424
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47;
                                   Score 24; DB
Pred. No. 47;
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Pred. No.
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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nes 5; Conserv
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RiHatakeyama, K.; Asai, Y.; Uchida, Y.; Kobayashi, M.; Terasawa, M.; Yukawa, H. Biochem. Biophys. Res. Commun. 239, 74-79, 1397
A;Title: Gene cloning and characterization of maleate cis-trans isomerase from Alcaligen A;Accession: UCS709; MUID:98005083; PMID:9345272
A;Accession: UCS709
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-253 <HAT>
A;Cross-references: UNIPROT:024766; DDBJ:AB005051; NID:g2575786; PIDN:BAA23002.1; PID:g2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: C71546
R;Stephens, R.S; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable glucose-6-phosphate dehyrogenase (devb family) - Chlamydia trachomatis (serotyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:084189; GB:AE001292; GB:AE001273; NID:g3328586; PIDN:AAC6777
A,Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                           Species: Alcaligenes faecalis
Date: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 09-Jul-2004
Accession: JC5709; PC4412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-25 <HA2>
C;Comment: This enzyme catalyzes the conversion of maleate to fumarate.
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                                        Indels
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cell division inhibitor minD - Escherichia coli (strain K-12)
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0
                                                                                                                                                                                                                                                                                                                                    - Alcaligenes faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: Alcaligenes faecalis maleate isomerase
C;Keywords: cis-trans-isomerase
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100.0%; Pred. No. 83;
tive 0; Mismatches
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100.0%; Pred. No. 8
          100.0%;
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C;Superfamily: yeast SOL3 protein
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                       maleate isomerase (EC 5.2.1.1)
                                        5; Conservative
          Similarity
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A;Molecule type: DNA
                                                                                                       1 LKAMD
                                                                                                                                                                LKAMD
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      Best Local
Matches
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C;Species: Sacillus subtilis
C;Species: Sacillus subtilis
C;Species: Sacillus subtilis
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Broon, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Musell
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurite, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell
K; Mathors: Lauber, J.; Lazarevic, V.; Eee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell
K; Mathors: Schleich, S.; Schroeter, R.; Scoffone, R.; Sadioch, Y.; Sado, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, R.; Sekiguchi, J.; Sekwaka, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Tarpstra, P.; Tognoni, A.; Tosako, V.; Volityama,
T.; Winters, P.; Wi
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alpha-1-B-glycoprotein - North American opossum (fragments)
alpha-1-B-glycoprotein - North American opossum (fragments)
clybecies: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu Cispecies: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu Cispecies: Didelphis virginiana (North American opossum sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
Cistanession: A42013
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum A;Reference number: A42013
A;Reference number: A42013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-237 <CAT-
A;Residues: 1-237 <CAT-
A;Cross-references: UNIPROT:Q28359; GB:J05356
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:O06732; GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12928.
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                        Length 210;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rosidues: 1-210 <SAN-
A;Cross-references: UNIPROT:P93525; EMBL:Y09874; NID:e1012757
A;Experimental source: variety Tx430; leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                     DB 2;
69;
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                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                     100.0%; Score 24; 100.0%; Pred. No.
                                                                                                                                                                                                                                Best Local Similarity 100. Matches 5; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             28 LKAMD 32
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R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-270 <STO>
A;Cross-references: UNIPROT: P18197; GB:AE005174; NID:g12514869; PIDN:AAG56026.1; GSPDB:G
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Species: Escherichia coli [imported] - Escherichia coli (strain O157:H7, substrain RI C, Species: Escherichia coli coli (strain O157:H7, substrain RI C, Species: Escherichia coli (strain O157:H7, substrain RI C, Bate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C; Accession: Espossy Respander, R.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C.G. gaaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 Myrithe: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomaly Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-270 «HAY»
A;Cross-references: UNIPROT: P18197; GB:BA000007; PIDN:BAB35092.1; PID:g13361133; GSPDB:C
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                    cell division inhibitor minD - Escherichia coli (strain O157:H7, substrain EDL933)
                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F86695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: F85695
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89;
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Pred. No. 89;
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100.0%; Pred. No. 89;
iive 0; Mismatches
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        LKAMD 113
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                                                                               C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: B31877; D64863
R;de Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
Cell 56, 641-649, 1989
A;Title: A division inhibitor and a topological specificity factor coded for by the mini A;Reference number: A31877; MUID:89136010; PMID:2645057
                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-270 < DEBA
A; Residues: 1-270 < DEBA
A; Cross-references: UNFROT: P18197; GB:J03153; NID:g146865; PIDN:AABS9062.1; PID:g146867
A; Cross-references: Unrkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1455-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
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S.Speciess: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002.
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C; Accession: AH0724
C; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Anule, S.; O'Gaora, P.
Anule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-270 <BLAT>
A,Cross-references: GB:AE000216; GB:U00096; NID:g1787417; PIDN:AAC74259.1; PID:g1787423;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Description: a membrane ATPase required for correct placement of cell division site AFONCE: minC and minD act in concert to form an inhibitor capable of blocking formation ion found between fis2 and minCD c; Superfamily: cell division inhibitor minD c; Superfamily: cell division control; nucleotide binding, P-loop F;10-17/Region: nucleotide-binding motif A (P-loop) P;16/Binding site: ATP (Lys) #status predicted
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A;Reaidues: 1-270 <PAR>
A;Reaidues: 1-270 <PAR>
C;Genetics: GB:AL513382; PIDN:CAD05498.1; PID:g16503002; GSPDB:GN00176
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title: The complete genome sequence of Escherichia coli K-12. Reference number: A64720; MUID:97426617; PMID:9278503. Accession: D45863. Accession: D48863. Accession: D48863.
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Alternate names: septum site-determining protein minD; Species: Escherichia coli
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100.0%; Pred. No. 89;
ive 0; Mismatches
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C; Superfamily: cell division inhibitor minD
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A; Status: preliminary
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Length 270;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 18:18:07; Search time 38.2 Seconds (without alignments) 67.026 Million cell updates/sec

US-10-047-945-3

1 LKAMD 5 Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	O9tr78 didelphis m				Ξ.	Q82k17 streptomyce			Q8yyg6 anabaena sp	Q93ce7 anabaena va	Q8gu99 oryza sativ		Q8xjc6 clostridium	Q721b6 thermus the	-	Q8hz75 didelphis m		Q889v2 pseudomonas	Q88q16 pseudomonas	Q9hwf4 pseudomonas	Q9i2x8 pseudomonas	Q655r8 oryza sativ	Q8wmu8 eulemur ful	Q8wmu9 eulemur ful	Q8wnn7 varecia var	Q8wnn8 varecia var	P00717 cygnus atra	Q8yh02 brucella me	006732 bacillus su		Q8nie7 glomus intr
																												CYGAT				
	Ω	09TR78	027566	Q72NV8	Q72TL6	Q6MJ74	Q82K17	Q8F7M0	Q80VT8	Q8YYG6	<b>Q93CE7</b>	Q8GU99	054772	QBXJC6	Q72LB6	Q8EQE9	<b>Q8HZ75</b>	037950	Q889V2	Q88QL6	Q9HWF4	Q912X8	Q655R8	QBWMUB	QBWIMU9	Q8WNN7	Q8WINB Q	LYG CY	Q8YH02	006732	Q9AGS2	Q8NIE7
	DB	~	~	~	N	N	~	~	7	~	~	7	~	7	~	~	N	N	N	N	~	~	7	~	~	~	~	-	~	~	N	0
		17	25	29	62	99	69	69	92	98	66	107	120	120	125	133	140	142	144	144	144	145	166	180	180	180	180	185	202	213	226	227
عد	Query Match Length	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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	Q8nj36 glomus intr	glomus		P93525 sorghum bic		Q62ww5 bacillus li		O24766 alcaligenes		Q9pkk7 chlamydia m		Q651h4 bacillus li	Q9vwa8 drosophila
3NJ35	3NJ36	28NJ37	55N09	993525	34WD9	S2WWS	29F155	24766	92501	PGL CHLMU	PGL_CHLTR	55LH4	'RG1_DROME
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227	227	227	229	235	245	247	251	253	254	256	256	256	262
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24	24	24	24	24	24	24	24	24	24	24	24	24	24
32	33	34	35	. 36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
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01-JUN-2003
01-JUN-2003
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TO PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;

NA Mascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,

TO B.L., Harke D.A., Verjovski-Almeida S., Hartskeerl R.A.,

Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,

Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,

Perro E.S., Ferro M.T., Furlan L.R., Gamberini M., Giglioti E.A.,

Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.T.,

Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,

de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,

A. Siqueira W.J., Sommer P., Teai S.M., Simpson A.J.G., Ferro J.A.,

Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;

T. "Comparative genomics of two Leptospira interrogans serovars reveals

"T. "Comparative genomics of two Leptospira interrogans serovars reveals
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                                                                                                                                                                                                                                                                               Copenhageni).
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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Bacteria, Spirochaetes, Spirochaetales, Leptospiraceae, Leptospira.
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                                                  Length 52;
                                                                           Indels
 1 1
52 52
52 AA; 5818 MW; CCC3C65E75DBA935 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insights into physiology and pathogenesis."; cteriol. 186:2164-2172(2004).
                                                 Query Match 100.0%; Score 24; DB 2; Best Local Similarity 100.0%; Pred. No. 95; Matches 5; Conservative 0; Mismatches 0
                                                                                                                                                                                         59 AA
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OrderedLocusNames=LIC12721;
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                            12 LKAMD 16
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05-JUL-2004
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Nascimento A.L.T.O., Ko.A.L., Martins E.A.L., Monteiro-Vitorello C.B., Andrewcaracovic, D. Martins E.A.L., Monteiro-Vitorello C.B., Andrewcaracovic, D. Martins E.A.L., Monteiro-Vitorello C.B., Andrewcaracovic, Monteira M.C., Menck C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H., Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R., Goldman G.H., Goldman M.H.S., Harakava R.T., Nuramae E.B., Junqueira-de-Azevedo I.L.M., Kimura E.T., Kuramae E.B., Lemos B.G.M., Lemos M.V.F., Narino C.L., Nunes L.R., A Goliveira R.C., Pereira G.G., Reis M.S., Schriefer A., Gamargo L.B.A., Kitalina J.P., Setubal J.C., Van Sluys M.A., Comparative genomics of two Leptospira interrogans serovars reveals T. Comparative genomics of two Leptospira interrogans serovars reveals to J. Bacteriol., 186:2164-217212004).

E.B.B., AB017291, AAS69612.1;
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"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from perspective.";
Science 303:689-692(2004).
EMBL: BXB42554; CAE80687.1; -.
CCmplete proteome.
SEQUENCE 66 AA: 8142 MW; 04D5D62C458E6ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bdellovibrio bacteriovorus.
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales;
Bdellovibrionaceae, Bdellovibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003346; Transposase_20.
Pfam; PF02311; Transposase_20; 1.
Complete proteome.
SEQUENCE 62 AA; 7499 MW; C79940D851F0CAC2 CRC64;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=Bd2909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AA
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Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 24; DB 2; Length 98; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
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Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Ventral prostate;
Oram S.W., Haleem R., Cai X., Cyriac J., Wang Z.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX195741; AAO40742.1;
SEQUENCE 92 AA; 10910 MW; OC406A170449BC19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome, Iron, Iron-sulfur, Metal-binding. SEQUENCE 98 AA, 10555 MW, 6D2CB4906B892AEE CRC64,
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GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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DNA Res. 8:205-213 (2001).
BBB, AP003583; BAB72841.1; -.
PIR; AI1916; AI1916.
                                                                                                                                                  92 AA
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OrderedLocusNames=asl0884;
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5, Conservative
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les 5; Conservative
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  1 LKAMD
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MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Pu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-G., Jia J., Tu Y.-F.,
Jiang J.-X., Gu M.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                            Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitlis."; Nat. Biotechnol. 21:526-531(2003).
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
VOSI_TaxID=173;
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.221433198;
Omura S., Ikeda H., Ishikawa J., Hananco A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
             OrderediccusNames=SAV2586;
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 AA; 7895 MW; C2E205A5D684D1F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                           Streptomycineae; Streptomycetaceae; Streptomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; DB 2; L
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                    STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 422:888-893(2003).
EMBL; AE011276; AAN48123.1; -.
Complete proteome.
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Hypothetical protein.
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hes 5; Conserv
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STRAIN=56601 / Ser
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RESULT 7

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Gaps

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Matches

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              5; Conservative
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Best Local Similarity
                                                                                                                      [1] SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      89 LKAMD 93
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                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMD 5
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                                                                                               NCBI_TaxID=1140;
                                                                                                                                                           STRAIN=PCC 7942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1502;
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05-JUL-2004
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                     Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=1172;
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100.0%; Pred. No. 2.18+02;
Wismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                     Schiefer W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu S., Xu Z., Xue H.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ495798; CAD44621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA; 11685 MW; 4899ACD54BE73D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                      EMBL; AFG10434; ADL05047.1; --
HSSP; P80106; 1E9M.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005189; F:electron transport; IEA.
InterPro; IPR001041; Ferredoxin.
Fram; PR00111; Ferz; --
Iron; Iron-sulfur; Metal-binding.
SEQUENCE 99 AA; 10702 MW; EJE3CCBA7E8B892A CRC64;
                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 24; DB 2; L
100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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                                                                            PRT;
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Best Local Similarity 100.,
Page 5; Conservative
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Best Local Similarity 100..
                                                                            PRELIMINARY;
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                                                                                                                                                                                                 Anabaena variabilis.
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 29413;
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SEQUENCE
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                               RESULT 10
Q93CE7
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Q54772
ID Q5477
AC Q5477
DT 01-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039). Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Thermus.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Hypothetical protein.
Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
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Phunitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59237; ABB82030.1; -.
Hypothetical protein:
SEQUENCE 120 Aa; 13515 MW; 91DDAF420ECFB6B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL; AP003192; BABB1540.1; -.

PROSITE; PS001190; CYTOCHROME_C; UNKNOWN 1.

SEQUENCE protecome; Hypotherical protein.

SEQUENCE 120 AA; 13909 MW; 063865C7F7FB1632 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical cytosolic protein.
OrderedLocusNames=TTC0143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
11-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein CPE1834.
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0;
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STRAIN=HTBB31;
MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                      Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus thermophilus."; Mat. Biotechnol. 22:547-553 (2004).

EMBL; AE017301; AAS80491.1; -.
InterPro; IPR002744; DUF59.
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01-MAR-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
02-vidine:deoxycytidine deaminase (EC 3.5.4.-).
Name-acdi, OrdertedLocusNames=0B1751;
0canobacillus iheyensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBL_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 24; DB 2; Length 125; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                125 AA; 13658 MW; 77B2D52BCA699896 CRC64;
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EMBL; AP004598; BAC13707.1; -. HSSP; P19079; JUTK.

GO; GO:00126; F:cytidine deaminase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0068270; F:sinc ion binding; IEA.

GO; GO:006870; F:cytidine metabolism; IEA.

InterPro; IPR005225; GVt deam tetra.

InterPro; IPR002125; GVT/deam tetra.

FIGRPANS; TICR01384; GVP/deam, 1.

FIGRPANS; TICR01384; GVP/deam, 1.

PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 133 AA.
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Best Local Similarity 100.
Matches 5; Conservative
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                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        Complete proteome
SEQUENCE 125 AA
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SEQUENCE 133 AA
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                                         PubMed=15064768;
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0880289
1D 0980289
DT 01-MA
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GenCore version 5.1.6
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protein search, using sw model ı OM protein

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US-10-047-945-3 24

1 LKAMD 5 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Beg Beg 98 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:* Database

geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

### SUMMARIES

Description	Aaw53842 N-terminu	Abb80224 Synthetic			Aaw53843 N-terminu	Abb80222 Synthetic	Abb80226 Synthetic	Abb80225 Synthetic	Aaw11575 N-termina	Aaw53841 N-terminu	Abb80223 Synthetic	Aab53797 Human col	Aab52152 Human sec	Aab52151 Human sec		Add29464 Mouse cae	Abp64620 Human ORF	Aab20323 Human pro	Aau33664 Pseudomon	Abu39905 Protein e	Abu42143 Protein e	Abu15537 Protein e	Abo72633 Pseudomon	Aau19728 Human nov	Aau87551 Novel cen
ID	AAW53842	ABB80224	ABB80228	ABB80227	AAW53843	ABB80222	ABB80226	ABB80225	AAW11575	AAW53841	ABB80223	AAB53797	AAB52152	AAB52151	ABG12903	ADD29464	ABP64620	AAB20323	AAU33664	ABU39905	ABU42143	ABU15537	AB072633	AAU19728	AAU87551
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Abp47948 Human pol Adc10910 Human ext Adi54866 Novel hum Aau87251 Novel cen Adi54566 Novel hum Abo81340 Pseudomon Aau87253 Novel cen Adi54568 Novel hum Adn17855 Bacterial Aau19847 Human nov Aau87553 Novel cen Abp48067 Human pol Adc11029 Human por Ads11888 Human the Ads11888 Human the Ads11888 Human the Ads11888 Human EST Ade40152 Human BST	Adn21642 Bacterial Adn24398 Bacterial
ABP47948 ADC10910 ADI54866 AAU87251 ADI54566 AAU801340 AAU19847 AAU19847 AAU1029 ADC11029 ADC11029 ADC511029 ADC511029 ADC511029 ADC511029 ADC511029 ADC511029	ADN21642 ADN24398
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# ALIGNMENTS

AAW53842 standard; peptide; 5 AA. N-terminus of opossum LTNF. (first entry) 08-JUL-1998 AAW53842; AAW53842 

LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.

Didelphis virginiana.

US5744449-A.

28-APR-1998.

96US-00657163, 03-JUN-1996; 93US-00058387. 94US-00310340. 10-MAY-1993; 22-SEP-1994;

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps FW, Lipps BV;

WPI; 1998-271108/24.

Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.

Claim 5; Col 13; 11pp; English.

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

Sequence 5 AA

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snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogran's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                           Length 5;
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                                                                                                         Score 24; DB 2; I
Pred. No. 1.8e+06;
                                                                                                                                             Mismatches
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                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic LINF, LT-5.
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                                       to horse proteins
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from requires a more complicated sandwich type ELISA
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Score 24; DB 7; Len
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                          100.0%;
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                                                              Conservative
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5; Conserva
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                            Query Match
                                               Local
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Sequence 8 AA;

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (ICTR) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & [IGE), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifiged immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemeic lugus erythematosus; SLB; rheumatoid arthritis; Sjogran's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
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9.
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                                        Length 8;
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serum requires a more complicated sandwich type ELISA
                              Score 24; DB 7; I Pred. No. 1.8e+06; Hismatches 0;
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Query Match
Best Local Similarity 100.
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Gaps

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Query Match 100.0%; Score 24; DB 7; Length 9; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 5; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                  LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the peptide of the invention. It is a Lethal Toxin Neutraliaing Pactor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Blapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
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                                                                                                        AAW53843 standard; peptide; 10 AA.
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94US-00310340.
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                                                                                                                                                                                                                                                                                     histamine reaction treatment
                                                                                                                                                                                                      N-terminus of opossum LTNF.
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22-SEP-1994;
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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-2002; 2002US-00047945
                          Synthetic LTNF, LT-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                 WO2003060471-A2.
                                                                                                                                                                                                                                                                                                                               24-JUL-2003
                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient.
  The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gg), nerve growth factor (NGF), insulin, myoglobin and/or adenosinse deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, clabetes, autoimmune disease (e.g. erythematosus (SLE). Theumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, c.g. Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins
                                                                                                                                  Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren; syndrome; Reiter's syndrome; Srayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be assayed by a simple ELISA test, whereas an assay of proteins from
serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 24; DB 7; Length 10; Similarity 100.0%; Pred. No. 25; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 3; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2003; 2003WO-US001044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2002; 2002US-00047945
                                              (first entry)
                                                                                            Synthetic LINF, LT-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-636703/60
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                   WO2003060471-A2.
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                                                                                                                                                                                                                                                            saliva; ELISA,
                                              06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2003.
                                                                                                                                                                                                                                                                                                          Synthetic.
ABB80222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient,
                                                                                                                                                                                                                                      Graves'
                                                                                                                                          Lethal
                                                                                                                                                                                                              SLE;
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e.g.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTME) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, at Addison's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an entilegram that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 AA;
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Gaps

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ABB80226 standard; peptide; 11 AA.

1 LKAMD 5 LKAMD 5

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06-NOV-2003 (first entry)

ABB80226;

Didelphis virginiana.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosinase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. aethma, allabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, at Adisease or Hodgin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins and the protein serum that is the compared to blood collection for serum. Saliva are contribugation to separate serum saliva proteins.
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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lethal toxin neutralising factor, LTNF, opossum; bee toxin, scorpion toxin, plant toxin; bacterial toxin; venom; sting; snake bite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                  14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                          14-JAN-2002; 2002US-00047945.
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                                                                                                                                                                                                                                                                                                                                                                                     Lipps BV, Lipps FW;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 AA;
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                                                                                               saliva; ELISA
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20-MAR-1997
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                                                                                                                                     Synthetic.
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1D AAW1

XC AAW1

XX AAW1

XX 25-M

DT 20-M

XX N-Leth

XW Leth

XW BCOF
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The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-WAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ent of victims of bee or scorpion stings or plant or bacterial - by admin. of lethal toxin-neutralising factor or its N-terminal
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100.0%; Pred. No. 37;
tive 0; Mismatches
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                                                                                                                                                                                                     94US-00310340.
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94US-00310340.
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Best Local Similarity
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LIPPS F W.
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22-SEP-1994;
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Matches
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                                                                                                                           This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogran's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
                                                                  Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                      100.0%; Score 24; DB 2; Length 15; 100.0%; Pred. No. 37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80223 standard; peptide; 15 AA.
                                                                                                       Claim 1; Col 11; 11pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic LINF, LT-15
                       Lipps BV;
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                                              WPI; 1998-271108/24
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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(LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                          to horse proteins
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                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                            1 LKAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           saliva; ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                      Lipps FW,
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor factor (IMTR) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, dalsease or Hodgin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointeetinal; nephrotropic; antinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
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infectious disease; cardiovascular disorder.
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Claim 3; Page 3; 24pp; English.
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nes 5; Conserv
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the preteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The color disorders and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, roll infectious diseases, and cardiovascular disorders. AAC9874 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein BLAST search protein SEQ ID NO: 108.
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 24; DB 3; Length 42;
100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100...
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LKAMD 32
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The invention relates to the isolation of genes AAC96900-C96947 encoding the human secreted proteins AAB52104-B52150. This sequence was used as a query sequence for BLASTX searches. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies

Disclosure; Page 447; 478pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of genes AAC96900-C96947 encoding the human secreted proteins AAB52104-B52150. This sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune themolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis,
                  of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epileps; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
and (ant)agonists are useful in the diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB52151 standard; protein; 70 AA.
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Matches 5; Conservative
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal carivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food suppliement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
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rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                  Length 70;
                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #12894.
                                                                                                                                                                                                                                                                                                                                                                             ABG12903 standard; protein; 105 AA.
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23-AUG-2000; 2000US-00649167.
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N-PSDB; AAS77090.
                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                           Sequence 70 AA;
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ABG12903
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CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 105 AA;
Query Match
Best Local Similarity 100.0%; Score 24; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 LKAMD 5
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Search completed: May 26, 2005, 18:36:55 Job time : 46 Becs

29 LKAMD 33

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Sequence 5, Appli
Sequence 2, Appli
Sequence 1337, Ap
Sequence 1337, Ap
Sequence 10123, A
Sequence 10123, A
Sequence 148579,
Sequence 41212, A
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                                                                                                                                           May 26, 2005, 18:43:39 ; Search time 32.8 Seconds (without alignments) 52.587 Million cell updates/sec
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Sequence 6,
Sequence 1,
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-156-761-10123
US-10-424-599-187934
US-10-424-599-148579
US-10-767-701-41212
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US-10-047-945-7
US-10-047-945-6
US-10-047-945-1
US-10-047-945-5
US-10-047-945-5
US-10-047-945-4
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                                                                                                                                                                                                                                                                                                                                                                                                                            1462099 seqs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Sequence 34493, A Sequence 1980, Appl Sequence 27576, Sequence 2160, Appl Sequence 43461, Appl Sequence 43461, Appl Sequence 378, Appl Sequence 378, Appl Sequence 5789, Appl Sequence 5789, Appl Sequence 5789, Appl Sequence 571, Appl Sequence 581, Appl Sequence 152, Appl Sequence 152, Appl Sequence 152, Appl Sequence 7631, Appl Sequence 152, Appl Sequence 7631, Appl Sequence 7	35, At 665, At 15452, At 15452, At 171, Apr 74006,
16 US-10-767-701-34493 15 US-10-449-857A-40 15 US-10-449-857A-40 15 US-10-424-599-181694 15 US-10-424-599-183694 15 US-10-424-599-183694 15 US-10-282-122A-70167 15 US-10-282-122A-70167 16 US-10-282-122A-70167 17 US-09-764-875-1069 17 US-09-764-875-1071 18 US-09-764-875-771 18 US-09-764-875-771 19 US-09-764-875-771 11 US-09-764-875-771 11 US-09-764-875-771 12 US-09-764-875-771 13 US-09-764-875-771 14 US-09-764-875-771 15 US-10-125-540-497 16 US-10-125-540-497 17 US-09-764-875-771 18 US-09-764-875-771 19 US-09-764-875-771 11 US-09-764-875-771 12 US-09-764-875-771 13 US-09-764-875-771 14 US-10-125-540-497 15 US-10-136-493-325 15 US-10-369-3433-325	(10-965-898-35 9-764-875-66 10-767-701-43 10-067-989-4 10-067-989-4 10-282-122A-7
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# ALIGNMENTS

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RESULT 6
US-10-047-945-4
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        Sequence 7, Application US/10047945
Publication No. US2003015755541
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE: 2002-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10047945
Publication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
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100.0%; Pred. No. 1.3e+06;
iive 0; Mismatches 0;
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Pred. No. 1.3e+06;
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100.0%; Pred. No.
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CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
FRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
LENGTH: 9
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7
SOFWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
LENGTH: 8
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US-10-047-945-1
; Sequence 1, Application US/10047945
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                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-047-945-6
US-10-047-945-7
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; Publication No. US20030157555A1
; Publication No. US20030157555A1
; GENERAL INPORMATION:
    APPLICANT: LIPPS, BINIB V.
; APPLICANT: LIPPS, BINIB V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: UGBS) INPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER:
; PRIOR PELLING DATE: 2002-01-14
; PRIOR FILING DATE: 2002-01-14
; ROWBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANIEM: Artificial Sequence
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: U(GE) IMPLICATED DISORDERS
CURRENT PAPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR PILING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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Sequence 1337, Application US/09925299

Publication No. US20030040617A9

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFRENCE: PA102

FILE REPRENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT PILING DATE: 2001-08-10

FRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: Patentin Ver. 2.0

FROUTH OF 1337
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                                                                                               CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05883
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver: 2.0
LENGTH: 42
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ORGANISM: Homo sapiens
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28 LKAMD 32
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LOCATION: (7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4
APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (198) IMPLICATED DISORDERS

FILE REFERENCE: FWLPATO15US

CURRENT APPLICATION NUMBER: U$/10/047,945

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

LEGGID NO 4

LEGGID NO 4

LEGGID NO 4

LEGGID NO 5

TYPE: ...
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APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
CURRENT PAPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR PILLING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Publication No. US20030157555A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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LENGTH: 15
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LOCATION:
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 148579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41212, Application US/10767701
; Sequence 41212, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53335)B
; CURRENT APPLICATION NUMBER: US/10/767,701
                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_140719C.1.pep
US-10-424-599-187934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_105189C.1.pep
US-10-424-599-148579
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 24; DB 15;
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(70)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(86)
OTHER INFORMATION: unsure at all Xaa locations
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FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESQ ID NO 187934
LENGTH: 70
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
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Best Local Similarity
Matches 5; Conserv
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Sequence 187934, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongivei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                    LOCATION: (12)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                          ; LOCATION: (40); COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1337
                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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Similarity 100.0%; Pred. No. 1.4e+02;
5; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 10 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10123
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
SAPPLICANT: SHIBA, FADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-10-156-761-10123
Sequence 10123, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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28 LKAMD 32
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Sequence 34493, Application US/10767701
Fublication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Co. Yongwei
APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FIRE REFERENCE: 38-21 (53325)
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 34493
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| Sequence 40, Application US/1049857A
| Sequence 40, Application US/1049857A
| Publication W. US20040043931A1
| GENERAL INFORMATION:
| APPLICANT: Hershberg, Robert M. |
| APPLICANT: Horsen, Mancy A. |
| APPLICANT: Lodes, Michael J. |
| APPLICANT: Mohamath, Raodoh | TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE |
| TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL |
| TUTLE OF INVENTION: BOWEL DISEASE |
| CURRENT APPLICATION NUMBER: US/10/449, 857A |
| CURRENT FILING DATE: 2003-05-30 |
| NUMBER OF SEQ ID NOS: 89 |
| SEQ ID NO 40 |
| LENGTH: 105
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                                                                                                                                                                                                                                                         Query Match 100.0%; Score 24; DB 16; Length 98; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49505_1.pep
US-10-767-701-34493
                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C26778_1.pep
US-10-767-701-41212
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; OTHER INFORMATION: Unknown Bacterium
US-10-449-857A-40
CURRENT FILING DATE: 2004-01-29 WINDER OF SEQ ID NOS: 63128 SEQ ID NO 41212 LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                      TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                             1 LKAMD 5
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30 LKAMD 34
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54 LKAMD 58
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ORGANISM: Unknown
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US-10-767-701-34493
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Query Match
Best Local Similarity 100.0%; Score 24; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMD 5
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| Db 12 LKAMD 16
Search Completed: May 26, 2005, 19:17:35
Job time: 54.8 secs
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Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 21379, A
Sequence 33456, A
Sequence 33086, A
Sequence 30086, A
Sequence 11113, A
Sequence 7062, Ap
Sequence 7062, Ap
Sequence 7559, Ap
Sequence 25133, A
Sequence 4420, Ap
Sequence 1509, Ap
Sequence 1509, A
Sequence 14, Appli
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32.741 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-657-163A-2

US-08-657-163A-1

US-08-657-163A-1

US-08-657-163A-1

US-09-252-91A-21179

US-09-270-767-33456

US-09-270-767-48962

US-09-270-767-48962

US-09-949-016-8959

US-09-949-016-8959

US-09-949-016-11113

US-09-949-016-11113

US-09-949-016-11113

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US-09-989-019-162-4

US-09-968-927-4

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US-09-107-52A-38B1

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US-09-107-52A-3B1

US-09-107-52A-3B1

US-09-107-52A-3B1
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                                                                                                                                                                                                                                   513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       protein search, using sw model
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Perfect score:
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No.
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Sequence 10, Appl Sequence 1285, W Sequence 142, Appl Sequence 164, Appl Sequence 106, Appl Sequence 20, Appl	NIION	
US-09-733-524A-10 US-09-600-588-1 US-09-600-588-1 US-09-905-125A-142 US-09-905-125A-142 US-09-902-775A-142 US-09-903-603A-142 US-09-903-603A-142 US-09-903-603A-142 US-09-903-603A-142 US-09-906-1142 US-09-906-1142 US-09-906-618-142	RESULT 1  US-08-657-163A-3  Sequence 3, Application US/08657163A  PRICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS TITLE OF INVENTION: EMBODIMENTS OF PARTIPAL AND TITLE OF INVENTION: STATHENT CINYER AND THEIR TITLE OF INVENTION: STATHENT CINYER AND THEIR TITLE OF INVENTION: STATHENT FOR ENVENOMATION NUMBER OF SEQUENCES: 3 CORRESPONDENCES: 3 CORRESPONDENCES: 3 COUNTRY: USA COUNTRY: USA STREET: 4509 MIMOSA DR. COUNTRY: USA COUNTRY: US	
W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Heren Britan Bri	2
000000000000000000000000000000000000000	APPLICATION: APPLICATION: INVENTION: INVENTI	YPE
**************************************	TITLE OF INVENTION:  APPLICANT: BINTE V. LIF APPLICANT: BINTE V. LIF TITLE OF INVENTION: EM TITLE OF INVENTION: UT NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: BINIE V. IS STREET: 4509 MIMOSA IC COMPUTER: TEXAS COMPUTER: TEXAS COMPUTER: TEXAS STATE: TEXAS COMPUTER: 198A WORD 2. CORRENT APPLICATION NUMBER: UT PILING DATE: 2.2 SEPTICATION NUMBER: PILING DATE: 10 MAY APPLICATION NUMBER: FILING DATE: 10 MAY ATTORNEY/AGENT INFORMATI NAME: JOHN R. CASPERR REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER: TELEFONDE: 713-482-25 TELEFONDE: 713-643-729 TELEFONDE: 713-643-729 TELEFONDE: 713-643-729 TELEFONDESS: SINGLE TYPE: AMINO ACID STRANDENNESS: SINGLE TYPE: AMINO ACID STRANDENNESS: SINGLE TYPE: PERFIDER HYPOTHETICAL: YES	ANTI-SENSE: N FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALINE V. LIPPS
STREET: 4509 MIMOSA DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 24; DB 1; Length 10; 100.0%; Pred. No. 4.2; ive 0; Mismatches 0; Indels
                                                           Length 5;
                                                                                             0; Indels
                                                       100.0%; Score 24; DB 1; I
100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM;
COMPUTER READABLE FORM;
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: PEPTIDE IN SEQ ID NO: HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28 198
REFERENCE/DOCKET NUMBER: FWL-PATTELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                        Sequence 2, Application US/08657163A
Patent No. 5744449
                                                                                                                                                                                                                                                                                                                                                                                    AUDRESS:
LIREET: 4509 MINOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: Us.
ZIP:
                                                                                             .
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID STRANDEDNESS: SIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINEAR
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                 1 LKAMD 5
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         US-08-657-163A-3
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Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
COTTY: BELLATRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INFERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: PLATY AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB COMPUTER: 1BM COMPATIBLE OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1 SOCTWARRE: MS WORD 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/310,340A FLILNG DATE: 2.2 SEPTEMBER 1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION UNDMER: 08/058, 387 FILING DATE: 10 MAY 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPOSSUM SERA: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORGANISM: DIDELPHIS VIRINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: WILD INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 77401
US-08-310-340A-1
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VS-09-252-991A-21379

VS-09-252-991A-21379

VS-09-252-991A-21379

Sequence 21379, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-17

NUMBER OF SEQ ID NOS: 33142

LENGTH: 145

LENGTH: 145

LENGTH: 145

CORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
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Patent No. 6703491

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-034

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 33456

LENGTH: 166
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           AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 24; DB 4; Length 166; Best Local Similarity 100.0%; Pred. No. 81; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 24; DB 4; Length 145; 100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                           h 100.0%; Score 24; DB 1; Length 15; Similarity 100.0%; Pred. No. 6.4; 5; Conservative 0; Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100 Matches 5; Conservative
PUBLICATION INFORMATION: AUTHORS: JONAS PERALE
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
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US-09-270-767-33456
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                                                                                                          RESULT 4
US-08-657-163A-1

Sequence 1, Application US/08657163A

Fatent No. 5744404

GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

TITLE OF INVENTION: SYNTHETIC LINFS AND THEIR

TITLE OF INVENTION: SYNTHETIC LINFS AND THEIR

TITLE OF INVENTION: UTILITY AS IREATMENT FOR ENVENOMATION

WUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE: BINIE V. LIPPS

STREET: 4509 MIMOSA ND

CITY: BELLIANT
                       DB 1; Length 15;
                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN: WILD INJUDIAL ISOLATE: TEXAS WILD INJUIDIAL ISOLATE: TEXAS WILD DEVELOPMENTAL STAGE: ADULT HAPLOTYPE: TISSUE TYPE: BLOOD CELL TYPE: CELL LINE: ORGANELLE: IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1: LIMERARY: CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77401
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTEM: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FWL-PAT-US-011
                    Query Match 100.0%; Score 24; Best Local Similarity 100.0%; Pred. No. Matches 5; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN IN SEQ ID NO: HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PATTELECOMMUNICATION INFORMATION:
TELECHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                     LUNESS:
LEET: BINIE V. LIPPS
CITY: BELLAIRE
STATE: TEXAS
COUNTRY:
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
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PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 30086 LENGTH: 182
                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30086
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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US-09-949-016-7062
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US-09-949-016-8959
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic 3226-094

CURRENT APPLICATION NUMBER: 185/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 33745

LENGTH: 174
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic 3126-094

CURRENT APPLICATION NUMBER: 05/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 48962

LENGTH: 174
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100.0%; Score 24; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                      Sequence 33745, Application US/09270767 Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48962
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Best Local Similarity 100.
Matches 5; Conservative
                                                                    17 LKAMD 21
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Sequence 7062, Application US/09949016

Sequence 7062, Application US/09949016

Falent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL 1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231, 768

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOFTWARE: PESESEQ for Windows Version 4.0

SEQ ID NO 7062
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SEQ ID NOS: 207012

SOFTWARE: PSESEQ for Windows Version 4.0

SEQ ID NO 8959

LENGTH: 192
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100.0%; Score 24; DB 4; Length 182; 100.0%; Pred. No. 89; 0; Indels ive 0; Mismatches 0; Indels
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FOR DIAGNO
                                                                                                                                                                   Sequence 4560, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
ENGLARIE LINDORGETTE-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
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Sequence 4420, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CUNKNOWN>
OPERATING SYSTEM: «UNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/095131
                                                                                                                                                                                                                                                                                                     FILE REPERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR PILING DATE: 1997-07-02
NUMBER: OF SEQ ID NOS: 5322
SEQ ID NO 4560
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4560
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CORRESPONDENCE ADDRESS:
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STATE: Massachusetts
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Best Local Similarity 100.
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                                                   111 LKAMD 115
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Reith Weinstock et al
APPLICANT: Reith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                              Sequence 11113, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR PELICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2070012
SOFTWARE: FasteseQ for Windows Version 4.0
LENGTH. 192
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; Patent No. 6747137
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                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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| LKAMD 6
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j TYPE: PRT

   ORGANISM: Human
US-09-949-016-8959
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US-09-949-016-11113
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TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4420:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                             NAME/KEY: misc_feature;
CCATION: (B) LOCATION 1...284;
SEQUENCE DESCRIPTION: SEQ ID NO: 4420:
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60 LKAMD 64
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Search completed: May 26, 2005, 19:08:39 Job time : 12.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 18:26:23; Search time 18:96 Seconds (without alignments) 60.897 Million cell updates/sec

US-10-047-945-4 69

Title: Perfect score:

1 LKAMDPTPPLWI 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	alpha-1-B-glycopro	hypothetical prote	hydroxymethylgluta	TATA-binding prote		ρ	fasciclin I precur	immunoglobulin-lik	probable acyl-CoA	lantibiotic Peps b	micofilarial sheat	proline-rich sheat	two-component resp	Xaa-Pro dipeptidas	probable beta-gluc	probable membrane	dprA protein [impo	gene 65 protein -	hypothetical prote	hypothetical prote	major structural n	beta-galactosidase	protein T24H7.5a [	hypothetical prote	protein T24H7.5b [	rifamycin polyketi	renin (BC 3.4.23.1	renin (EC 3.4.23.1	hypothetical prote
SUMMARIES	3 ID	2 A42013	E75099	1 A31898	2 A54063	D71194		A29900	2 T09402		S58360	S26854	2 A40525	2 C70045	2 C83867			2 F87552 ·	s S31010	: T16406	: T16659			2 D88175		2 C88175	: T17466	REMSS	REMSK	: C71820
	Length DB	237		932 1				•	1327	•	967	205	205	225		260	609	365		426	492			1212 2		1454	1728 2	401	402	259 2
allo	Query Match	75.4	62.3	62.3	62.3	6.09	ö	6.09	60.9	59.4	59.4	58.0	58.0	58.0	58.0	58.0	58.0	•	56.5	56.5	o	ဖ	φ	56.5	φ	ė.		'n.	55.8	55.1
	Score	52	43	43	43	42	42	42	42	41	41	40	40	40	40	40	40	39.5	39	39	39	39	39	39	39	39	39	38.5	8	38
	Result No.	1	7	m	4	'n	φ	7	ω	O	10	11	12	13	14	, 15	16	17	18	19		21	22	23	24	25	26	27		29

hypothetical prote	peroxidase (EC 1.1	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable nucleopor	steroid hormone re	hypothetical prote	hypothetical prote	hypothetical prote	similar o transcri	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
B70710	T10945	T22794	T29187	C85438	E97580	S62497	805979	T33606	. AB2368	G72520	AE1681	AG2568	A83045	C70829	C87585
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347	364	099	792	896	1127	1325	1443	1145	98	116	142	144	149	162	212
55.1 347		55.1 660		55.1 896	_	_	55.1	54.3	53.6	53.6	53.6	53.6	53.6		
38 55.1 347				55.1	55.1	_	55.1	54.3	53.6		53.6	53.6	53.6		

# ALIGNMENTS

	RESULT 1 A42013	
	alpha-1-B-glycoprotein - North American opossum (fragments) C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu	nssoc
	C;Date: 10-Jul-1992 #Bequence_revision_10-Jul-1992 #text_change 09-Jul-2004 C;Accession: A42013	
	R/Catanese, J.J.; Kress, L.F. Biochemistry 31, 410-418, 1992	
	A; Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum A: Reference number: A42013: MUID:92118834; PMID:1731898	hum o
	A;Accession: A42013	
	A:Status: preliminary A:Molecule type: mRNA	
	A; Residues: 1-237 < CAT>	
	A;Cross.references: UNIPROT:Q28359; GB:J05356 C;Keywords: glycoprotein	
	75.48;	
	Hest Local Similarity 83.3%; From. No. 0.26; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
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1 LKAMDPTPPLWI 12 ||||| || ||| LKAMDTTPRLWI 12 셤 ઠે

C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 hypothetical protein PAB1590 - Pyrococcus abyssi (strain Orsay)

C. Accession: E75099
R. anonymous, Genoscope submitted to the EMBL Data Library, July 1999
R. anonymous, Genoscope submitted to the EMBL Data Library, July 1999
A. Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A. Accession: E7509
A. A. Accession: E7509
A. Status: preliminary
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-695 < KAM>

A;Cross-references: UNIPROT:Q9UZG1; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5009
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1590 Query Match 62.3%; Score 43; DB 2; Length 695; Best Local Similarity 60.0%; Pred. No. 28; Msmatches 5; Conservative 2; Mismatches 2; Indels

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Gaps

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Tue May 31

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309 KELDPTPPL 317
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                                                                                                                                                                                                                                                                                                                                           A/Accession: A31898 MUID:89054023; PMID:3192541
A/Accession: A31898
A/Accession: A21898
A/Accession: A21897
A/Accession: A21897
A/Accession: A21897
A/Accession: A21897
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A/Accession: A21898
A/Accession: A21898
A/Accession: A21898
A/Accession: A21896
A/Accession: A2189
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C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Date: 0.2-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C.Accession: A54063
R.Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.
Science 1.23-941, 1994
A;Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding to c
A;Reference number: A54063
A;Accession: A54063
A;Acc
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentro C'Species: Strongylocentrotus purpuratus (purple urchin)
C'Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A31898; A28367
R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
B;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
A;Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduc
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hypothetical protein PH1828 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
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66.7%; Pred. No.
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A.Cross-references: FlyBase:FBgn0011836
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620 LSAMDDSPVLWI 631
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Matches 8; Conservative
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Matches 7
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchı Dux Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71194
A;Katusi preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-115 <KAWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-raferences: UNIPROT:059492; GB:AP000007; NID:g3236134; PIDN:BAA30947.1; PID:g325
A,Experimental source: strain OT3
A,Note: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
A;Experimental source: strain Nigg (MoPn)
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935
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A,Residues: 1-662 <ZIN>
A,Cross-references: UNIPROT:P10675, GB:M20544, GB:J03787, NID:g160846; PID:g160847
A;Cross-references: UNIPROT:P10675, GB:M20544, GB:J03787, NID:g160846; PID:g160847
R;Snow, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.;
Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988
A;Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t
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C;Superfamily: Chlamydia trachomatis hypothetical protein CT036
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llarity 77.8%; Pred. No. 22;
Conservative 1; Mismatches
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2; Mismatches
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Tantibiotic Pep5 biosynthesis protein pep8 - Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S66655; S58360
R;Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Kem R;Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Kem Riv. J. Biochem. 232, 478-489, 1995
A;Title: Nucleotide sequence of the lantibiotic Pep5 biosynthetic gene cluster and funct A;Reference number: S66651; MUID:96035882; PMID:7556197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Brugia pahangi
C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C;Accession: A40525; S18744
R;Selkirk, M.E; Yazdanbakhsh, M.; Freedman, D.; Blaxter, M.L.; Cookson, E.; Jenkins, R.
J. Biol. Chem. 26, 11002-11008, 1991
A;Title: A proline-rich structural protein of the surface sheath of larval Brugia filari
A;Reference number: A40525; MUID:91250404; PMID:1710216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT: Q54123; EMBL: Z49865; NID: 9945014; PIDN: CAA90025.1; PID: 99450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 826854
R;Selkirk, Washirk Data Library, February 1991
A;Reference number: 826854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proline-rich sheath protein Mf22 precursor - nematode (Brugia pahangi)
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Pred. No. 23;
1; Mismatches
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3; Mismatches
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Pred. No. 8
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milarity 54.5%;
Conservative 1
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Best Local Similarity 54.5
Matches 6; Conservative
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146 LTQQTPTPPIW 156
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102 IKALDTTNPIW 112
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A;Molecule type: DNA
A;Residues: 1-967 <ME2>
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A, Status: preliminary
A, Molecule type: DNA
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Cispecies: Thomson, N.R.; Mycobacterium light l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1327 ** MNZ>
A;Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:G2645889; PIDN:AAC52057.1; PID:G2
C;Genetics:
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A, Cross-references: UNIPROT: Q9CD82; GB: AL450380; NID: 913092512; PIDN: CAC29642.1; GSPDB: Q
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin-like protein IGSF1 - human
[Species Homo capiens (man)
[C.Species (man)
[C.Specie
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                                                                                                                                                                                                                                                     Length 662;
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A; Reference number: A94202; MUID:88276943; PMID:2839842
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84;
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Pred. No. 84;
0; Mismatches
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Pred. No. 61;
2; Mismatches
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Pred. No. 39;
1; Mismatches
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                                                                            A;Molecule type: mRNA
A;Residues: 25-42 <SNO>
A;Cross-references: EMBL:M20544; EMBL:J03787
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Best Local Similarity 58.3%;
Matches 7; Conservative
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104 LSELDGNPPLWI 115
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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A,Map position: Xq25
                                              A; Accession: A31817
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Score 40; DB 2; Pred. No. 23;

58.0%;

Query Match Best Local Similarity

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Search completed: May 26, 2005, 18:44:50 Job time: 19.96 sec8
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R; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4317, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A; Reference number: A83650; MUD; 20512582; PMID:11058132
A; Accession: C83867
A; Residuan Prope: DNA
A; Residuae: 1-406 < STOO
A; Residuae: 1-406 < STOO
A; Residuae: 1-406 < STOO
A; Experimental source: strain C-125
A; Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-225 <KUN> A;Cross-references: UNIPROT:032192; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15291.C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Accession: C83867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xaa-Pro dipeptidase BH1739 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
   Gaps
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                                                                                                                                                               regulator [YvqB] homolog yvqA - Bacillus subtilis
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F;52/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2; Length 406;
Pred. No. 49;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2; Length 225;
Pred. No. 25;
1; Mismatches 3; Indels
 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  idene: yvqA
;Superfamily: ompR protein; response regulator homology
 1, Mismatches
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
6; Conservative
                                                                      146 LTQQTPTPPIW 156
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                                    1 LKAMDPTPPLW 11
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R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul. Subnitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
A;Reference number: 214667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Residues: L-560 <ROU>
A,Residues: 1-560 <ROU>
A,Residues: L-560 <ROU>
A,Residues: L-560 <ROU>
A,Residues: L-560 <ROU>
A,Residues: L-560 <ROU>
A,Residues: Univar Columbia
A,Experimental source: cultivar Columbia
B,Experimental S, S,Experimental S, S,Experi
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A;Residues: 1-560 <STO>
A;Cross-references: GB:AE002093; NID:g3128191; PIDN:AAC16095.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02404; B84879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: At2g44490; F4II.30
A;map position: 2
A;Introns: 3/2, 33/3; 76/3; 102/1; 157/2; 242/3; 281/2; 354/1; 400/1; 438/2
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  probable beta-glucosidase homolog F4II.30 - Arabidopsis thaliana
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Pred. No. 69;
2; Mismatches
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Best Local Similarity 54...
Local 6; Conservative
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334 IKHVDPTQPTW 344
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                                                                     389 PSPPLWV 395
PTPPLWI 12
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Tue May 31 05:58:08 2005

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

May 26, 2005, 18:18:07; Search time 91.68 Seconds (without alignments) 67.026 Million cell updates/sec Run on:

US-10-047-945-4

1 LKAMDPTPPLWI 12 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched: Total number of hits satisfying chosen parameters:

1612378

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:* Database

1: uniprot_sprot:* 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	Description	1		Q8hz75 didelphis m		Q8hyx5 didelphis m		Q7qe48 anopheles g						Q8vm74 rhizobium s		Q9uzgl pyrococcus		_						_	Q6yid6 penaeus mon	-	P10675 schistocerc		-		Q9nv61 homo sapien	O9w3h5 drosophila
SOMPLAKIES	ΙD	Q9TR78	DM43_DIDMR	Q8HZ75	Q8HZ74	Q8HYX5	Q73ZB2	Q7QE48	Q833V1	Q7YQJ7	QBBXK6	Q18150	Y4VJ_RHISN	Q8VM74	Q846T8	Q9UZG1	HMDH_STRPU	TAF2 DROME	0594 <u>9</u> 2	Q7Q3Z4	Q8N6C5	Q6FB99	X306_CHLMU	Q7WLE6	Oexide	Q83WX7	FAS1_SCHAM	015070	Q8FNB0	Q6CS47	Q9NV61	ОЭМЗНБ
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	Length	17	291	140	291	314	227	370	128	467	242	477	351	354	360	695	932	1221	115	190	242	356	398	408	576	612	662	1437	51	66	125	165
	Match	100.0	100.0	87.0	87.0	75.4	72.5	66.7	65.2	65.2	•	63.8	62.3	62.3	62.3	62.3	62.3	62.3	6.09	6.09	60.9	6.09		6.09	•	60.9	6.09	6.09	59.4	59.4	59.4	59.4
	Score	69	69	9	9	25	20	46	45	45	44	44	43	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	41	41	41	41
11.000	No.	п	63	٣	4	ហ	ø	7	80	σ	10	11	12	13	14	15	16	17,	18	19	20	21	22	23	24	25	56	27	28	29	30	31

	Q7mtq9 porphyromon Q8mis3 didelphis m	Q9cd82 mycobacteri O9vqp4 drosophila	· ·		Q7nfil gloeobacter O6uxu0 homo sapien	Q00032 brugia paha
Q6UW07 Q9HBJ8	Q7MTQ9 Q8MIS3 Q9WQD3	Q9CD82 Q9VQP4	Q9GZ10 Q54123	Q7KU30 RRPL AHSV9	Q7NFĪ1 OGUXUO	Q00032
00	000	100	~ ~	2 4	0 0	7
212	344 504	707	856 967	1017	78 137	205
59.4 59.4	4. 4. 4	500.	59.4	59.4	58.0	58.0
14, 14	444	4 4	<b>4</b> 4	4 4	4 4 0 0	40
32	6. 6. 6. 4. 73. 6.	323	39	41	4 4 4 4	45

## ALIGNMENTS

Gaps SEQUENCE.
MEDIATE=9149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
MEDIATE=9149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;
"Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae.";
Toxicon 32:1237-1249(1994)
SEQUENCE 17 AA, 1947 MW; CBS5F840E73B2A2A CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment).
Didelphis marsupialis (Southern opossum).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
N.T. TaxID-9268; ö 100.0%; Score 69; DB 2; Length 17; 100.0%; Pred. No. 0.00027; tive 0; Mismatches 0; Indels 17 AA. PRT; Query Match
Best Local Similarity 100. PRELIMINARY; Q9TR78 ID Q9TR78 RESULT 1 

1 LKAMDPTPPLWI 12 1 LKAMDPTPPLWI 12 ઠે g

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16-0CT-2001 (Rel. 40, Created)
16-0CT-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Venom metalloproteinae inhibitor DM3.
Venom metalloproteinae inhibitor DM3.
Didelphis marsupialis (Southern opossum).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis. 291 AA. PRT; STANDARD; DIDMR DM43 DID P82957; RESULT 2 DM43 DIDMR 

SEQUENCE, AND MASS SPECTROMETRY. IISSUE=Serum;

MEDLINE=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;

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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9268;
                     NCBI_TaxID=9267;
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                  SEQUENCE
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP51-D (Fragment).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsuphalis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                 -!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IRR07110; Ig-like.
InterPro; IRR0711015; LEM_like.
Pfam; PF00047; ig. LEM_like.
PROSITE, PS50835; IG_LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Metalloprotease inhibitor; Repeat.
DOMAIN 12 79 Ig-like V-type 1.
DOMAIN 114 171 Ig-like V-type 2.
DOMAIN 191 288 Ig-like V-type 3.
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-i- PTM: N-glycosylated.
-i- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 69; DB 1; Length 291; 100.0%; Pred. No. 0.0055; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Martinez M.E., Pierce J.R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY131000; AAN06911.1; -.
                                                                                                                                                                                                                                                                                                                                                                           17A496227E69A65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 AA; 15297 MW; E19D071A76AA5A7F CRC64;
                                                                                                                                                                                                                                                                                                (GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
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Pred. No. 0.072;
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N-linked
N-linked
N-linked
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91.7%;
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Best Local Similarity luv...
Best Local 2; Conservative
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Matches 11; Conserv
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 24 314 venom metalloproteinase inhibitor DM43b SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C., Domont G.B., Ho P.L., Perales J.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Didelphis maršupialis (Southern opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis
                                                                                                                                                                                                                                                                                                                                                                                       Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                     Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX131001; AAN06912.1; -.
HSSP; Q8NHE, 100X.
                                                                                                                                                                                                                                                                                                                                           291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venom metalloproteinase inhibitor DM43b precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 2;
Pred. No. 3.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 2;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY163806; AAN64698.1; -- HSSP; P24071; 10VZ.
                                                                                                                                                                                                                                                         SMART; SM00409; IG; 1.
PROSITE; PSS0835; IG_LIKE; 1.
NON TER 1 291
NON_TER 291 291
                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR003599; Ig.
InterPro, IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 1g; 1.
SMART; SM00409; 1G; 1.
PROSITE; PS50835; 1G_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.4%;
                                                                                                                                                                                       InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LKAMDPTPPLWI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPRLWI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 LKAMDTTPRLWI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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5 DPTPPLWI 12
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76 NPTPPLWV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
SEQUENCE 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; EF1825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M.
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Matches
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   ACCOS ON THE SECOND ON THE SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                         Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AE017233, AAS04008.1; -
                                                      Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 2; Length 370;
Pred. No. 37;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Contains 2 C2 domains.
                                                                                                                                                                                                                                                                                                                                                                               227 AA; 24027 MW; 952EA4962C0EE199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40989 MW; C558FDA3D5CD8D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgCP7225 (Fragment).
Name=agCG51396; ORFNames=ENSANGG0000014288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0016020; C:membrane; IEA.
GO:0008021; C:synaptic vesicle; IEA.
GO:0005215; F:transporte activity; IEA.
GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; D
Pred. No. 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%;
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                           OrderedLocusNames=MAP1691c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; 2.
C2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.5
Best Local Similarity 72.7
Matches 8; Conservative
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146 LAALDPRPPLW 156
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294 IRALDPTNPIW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKAMDPTPPLW 11
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 227 AA;
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                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=k10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=PEST
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Q7QE48;
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Q833V1
ID Q833
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XX MEDLINE-22753825; PubMed=12740363; DOI=10.1074/jbc.M303210200;

XA Jutabha P., Kanai Y., Hosoyamada M., Chairoungdua A., Kim D.K.,

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

Interpro, I
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                                                                                                                                                                                                                                                                                   Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=V583 / ATCC 700802;
MEDLINE=22550857; Pubmed=12663927; DOI=10.1126/8cience.1080613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA; 14458 MW; 43459A9BE814572F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Conserved domain protein.
OrderedLocusNames=EF1825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.2%; Score 45; DB 2; 58.3%; Pred. No. 69; ive 3; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.2%; Score 45; DB 2;
larity 75.0%; Pred. No. 18;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis.";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016952; AA081592.1;
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1 LKAMDPTPPLWI 12

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128 AA

PRT;

PRELIMINARY;

Q833V1

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched
library, clone:B330018M03 product:hypothetical Ebronectin type III
structure containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Adrenal gland; MEDLINE=20499374; PubMed=11042159; DOJ=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOJ=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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STRAIN-C5-FBL/6J; TISSUE-Adrenal gland;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Adrenal gland; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Mishia K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishinc T., Harada A., Yamamoto R., Mateumoto H., Sakayuchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikzwi Integrated sequence analysis (RISA) system-384-format sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Adrenal gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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STRAIN=CS7BL/6J; TISSUE=Adrenal gland;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                        PRT;
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:||| :||||:
255 IKAMIKSPPLWV 266
                                                                                                                                                                                                                        PRELIMINARY;
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Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagama A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SUBCEDIULAR LOCATION: Nuclear (By similarity).
-!- SUBCEDIULAR LOCATION: Outlear (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                      63.8%; Score 44; DB 2; Length 242; 77.8%; Pred. No. 50; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol N2;
Wilson R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid C25B8.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                           MGD; MGI:2444790; B930041F14Rik.
GO; GO:0016021; C:integral to membrane; TAS.
Hypothetical protein.
SEQUENCE 242 AA; 26120 MW; FD8FE24EB994F8F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nuclear hormone receptor family protein 120.
Name=nhr-120; ORFNames=C25B8.6;
                                                                                                                                                                                                                                                                                                                                                              477 AA.
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HSSP; P20393; 1A6Y.
                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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                                                                                                                                                                                                                                                      3 AMDPTPPLW 11
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Submitted (NOV-2002)
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Submitted (JUN-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormBase Consortium;
                                                                                                                                                                                                                                                                                   20 AVDPTPPGW
                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
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STRAIN=BR816:
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Q8VM74
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Matches
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Q846T8
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              GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0003700; F:reeroid hormone receptor activity; IEA.

R GO; GO:0003700; F:reeroid hormone feceptor activity; IEA.

R GO; GO:0006355; P:reeglation of transcription, DNA-dependent; IEA.

R InterPro; IPR000936; Hrmon recept 11g.

R InterPro; IPR000349; Str ncl.receptor.

R InterPro; IPR000349; VitD. receptor.

R Pfam; PF000149; Arrone recep; 1.

R Pfam; PF000105; zf-C4; 1.

R PRINTS; PR00350; VITAMINDR.

R SWART; SW00430; HOLI; 1.

R SWART; SW00430; HOLI; 1.
                                                                                                                                                                                                                                                                                                                        SWART; SM00399; ZRF_C4; 1.
PROSITE; PS00031; NUGLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 477 AA; 54900 MW; 9D16A8FF3BDC0241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beginning.";
Genome Res. 6:590-600(1996).
-!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Freiberg C., Perret X., Broughton W.J., Rosenthal A.; "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable 'sequenase': a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perret X.;
"Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.8%; Score 44; DB 2; Length 477; 54.5%; Pred. No. 1e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q53218;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-NUL-2004 (Rel. 44, Last annotation update)
Hypothetical 39.2 kDa protein y4vJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 AA
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EMBL, AE000101, AAB91898.1; -.
InterPro, IPR002103; Bac_luciferase.
InterPro, IPR011251; Luciferase_like.
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MEDLINE=96389014; PubMed=8796346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=y4vJ;
Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 54.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KAMDPTPPLWI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : |:||:||
18 KLLHPSPPMWI 28
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Matches
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0
Pfam; PF00296; Bac luciferase; 1.
Hypothetical proteIn; Monooxygenase; Oxidoreductase; Plasmid.
SEQUENCE 351 AA; 39158 MW; 866BDE3B8A40C88D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
NCBI_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBI TaxID=48291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.3%; Score 43; DB 2; Length 354; 85.7%; Pred. No. 1.1e+02;
                                                                                        Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luyene E., Swinnen E., Verreth C., Vlassak K., Dombrecht Vanderleyden J.;
Vanderleyden J.;
Submitred (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U26451, AAL61964.1; -.
Pfam; PF00296; Bac_luciferase; 1.
                                                                                    Score 43; DB 1; Length 351
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luyten B., Verreth C., Vanderleyden J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 AA; 39367 MW; 9D18A3F09BA70A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical adventurous gliding motility protein M.
                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative LuxA.
Rhizobium sp. (strain BR816).
                                                                                        62.3%;
85.7%;
                                                                                                           Local Similarity 85.7
hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                      167 PTPPIWI 173
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                                                                                                                                                                          6 PTPPLWI 12
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STRAIN=GES / OrBay;

MEDLINE=22511545; PubMed=12622808;

Cohen G.W., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch G., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Van der Cost J., Weissenbach J., Zivanovic Y., Forterre P.;

"An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.";

Mol. Microbiol. 47:1495-1512(2003).

ENRL, AJ248266, CAB50038.1; -.

PIR, F75099, E75099.

SEQUENCE 695 AA; 79999 MW; 371E0E402210F551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
                                                                                                                                             Gaps
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GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001915; Peptidase M48.
Interpro; Peptidase M48; I.
Hydrolase; Hypothetical protein; Metalloprotease; Protease; Zinc.
SEQUENCE. 360 AA; 40304 MW; 98AB27E93EAEC023 CRC64;
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                                                                                                         Ouery Match 62.3%; Score 43; DB 2; Length 360; Best Local Similarity 66.7%; Pred. No. 1.1e+02; Matches 6; Conservative 1; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-UJN-2003 (TYEMBLrel. 24, Last annotation update)
Hypothetical protein.
ORFNames=PAB1590;
                                                                                                                                                                                                                                                                                                         695 AA.
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561 ANDPKPPMWL 570
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Q9UZG1
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Search completed: May 26, 2005, 18:43:24 Job time : 92.68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

May 26, 2005, 18:17:22 ; Search time 103.2 Seconds (without alignments) 44.972 Million cell updates/sec

US-10-047-945-4 69

1 LKAMDPTPPLWI 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 08 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1990s:* geneseqn2001s:* geneseqn2001s:* geneseqn2002s:* geneseqn2003s:* geneseqn2003bs:* A_Geneseq_16Dec04:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	lon	Synthetic	N-termina	N-terminu	Synthetic	Synthetic	N-terminu	Synthetic	Synthetic	Enterococ	Novel hum	Novel hum		Human pro	HMG-COA r	TATA-bind	Drosophil	TATA-bind	Drosophil	Human pol	Human pit	Human pit	Streptomy	Breast ca	Human pro	Novel hum
,	Description	Abb80225	Aaw11575	Aaw53841	Abb80223	Abb80226	Aaw53843	Abb80222	Abb80227	Adh88053	Abg22890	Abg18144	Abb80228	Aam79784	Adm98800	Aar56496	Aaw06086	Aaw25029	Abb62618	Aao02179	Adb90591	Adb90617	Adh39800	Abr47496	Adp18673	Aau32796
SOMMAKIES	ID	ABB80225	AAW11575	AAW53841	ABB80223	ABB80226 ·	AAW53843	ABB80222	ABB80227	ADH88053	ABG22890	ABG18144	ABB80228	AAM79784	ADM98800	AAR56496	AAW06086	AAW25029	ABB62618	AA002179	ADB90591	ADB90617	ADH39800	ABR47496	ADP18673	AAU32796
	DB	7	~	~	7	7	7	7	7	7	4	4	7	4	80	N	7	~	4	4	7	7	8	9	œ	4
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de	Query Match	100.0	100.0	100.0	100.0	94.2	78.3	78.3	72.5	65.2	63.8	63.8	62.3	62.3	62.3	62.3	62.3	62.3	62.3	6.09	6.09	6.09	6.09	6.09	6.09	60.09
	Score	69	69	69		65	54	54	20	45	44	44	43	43	43	43	43	43	43	42	42	42	42	42	. 42	42
	Result No.	-1	7	m	4	ß	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abr12621 Human can Abr12017 Human can	Abr12854 Human can Abr12743 Human can	Abr11875 Human can Abr12121 Human can	Human	Human	Abr12738 Human can	Abr33125 Human can	Abr33383 Human can	Abr33116 Human can	Abr33427 Human can	Abr33363 Human can	Abb42105 Peptide #	Aam75798 Human bon	Aam62985 Human bra	Abb40295 Peptide #	Aam33978 Peptide #
ABR12621 ABR12017	ABR12854 ABR12743	ABR11875 ABR12121	ABR12948	ABR12294	ABR12738	ABR33125	ABR33383	ABR33116	ABR33427	ABR33363	ABB42105	AAM75798	AAM62985	ABB40295	AAM33978
	9 10 6	10 10 6	10 6	_	10 6	15 6	15 6	_	_	15 6	37 4		Ī	64 4	64 4
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26 27	7 7 8 8 8	30 31	32	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA. ABB80225 standard; peptide; 12 AA. 06-NOV-2003 (first entry) Synthetic LTNF, LT-12. ABB80225; ABB8022 

Synthetic.

WO2003060471-A2.

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

Gaps

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0; Indels

100.0%; Pred. No. 0.00041; ative 0; Mismatches 0;

12; Conservative

Matches

Best Local Similarity

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arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of victime of bee or scorpion stings or plant or bacterial toxins - by admin, of lethal toxin-neutralising factor or its N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lethal toxin neutralising factor; LTNP; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                              Score 69; DB 7; Length 12; Pred. No. 0.00033;
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                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                           Sequence 12 AA;
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20-MAR-1997
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                                                                                                                                                                                                                                      LTNF, lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
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100.0%; Pred. No. 0.00041;
ive 0; Mismatches 0;
                                                                                                              AAW53841 standard; peptide; 15 AA.
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94US-00310340.
                                                                                                                                                                                                                                                                                           histamine reaction treatment
                                                                                                                                                                                                           N-terminus of opossum LTNF.
                                                                                                                                                                          08-JUL-1998 (first entry)
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Best Local Similarity 100.
Matches 12; Conservative
12
                              LKAMDPTPPLWI 12
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LKAMDPTPPLWI
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Б. Х.
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(LIPP/) LIPPS
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                                                                                                                                            AAW53841;
                                                                              RESULT 3
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RESULT 4 ABB80223

100.0%; Score 69; DB 2; Length 15

Query Match

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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; disbetes; autoimmune disease; systemeric lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                  14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                 14-JAN-2002; 2002US-00047945
                                               Synthetic LTNF, LT-11.
                                                                                                                                                                                                                                                                                                                                                                                             Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                              (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                    WO2003060471-A2
                                                                                                                                                          saliva; ELISA
                                                                                                                                                                                                                                                   24-JUL-2003
                                                                                                                                                                                     Synthetic.
 The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insive growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE). Theumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an arti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collection that the proteins are centrifiqued immediately, whereas blood requires collection that the proteins are contrifiqued immediately, whereas blood requires collection that the proteins are contributed to the separate serum. Saliva
                                                                                                                    Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; diabetes; autoimmune disease; systemic lugue erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assayed by a simple ELISA test, whereas an assay of proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 7; I
Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 3; 24pp; English.
ABB80223 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                               14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                              14-JAN-2002; 2002US-00047945
                                                          (first entry)
                                                                                          Synthetic LTNF, LT-15
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                                           (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                 WO2003060471-A2.
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                                                                                                                                                                                                    saliva; ELISA
                                                            06-NOV-2003
                                                                                                                                                                                                                                                                                                24-JUL-2003
                                                                                                                                                                                                                                   Synthetic.
                              ABB80223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patient.
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (ISE), nerve growth factor (MGP), insulin, myoglobin and/or adenosines deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and tracting conditions with elevated serum ISE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva canlescent election that is specific for the protein. Saliva can be centrifuged immediately, whereas blood requires
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Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    time before centrifugation to separate serum. Saliva protéins
ssayed by a simple ELISA test, whereas an assay of proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be assayed by a simple ELISA test, whereas an ass
serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.2%; Score 65; DB 7; I
100.0%; Pred. No. 0.0013;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW53843 standard; peptide; 10 AA.
                                                                                                                                                         Claim 7; Page 4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assayed by a simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                 patient
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Gaps

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0; Indels

Mismatches

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Conservative 1 LKAMDPTPPLWI 12 

12;

Matches

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Similarity

ABB80226 standard; peptide; 11 AA.

ABB80226

ABB80226 ID ABB8 XX AC ABB8 RESULT 5

28-APR-1998

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (INTR) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MCF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Siogren's syndrome, Reiter's syndrome, Graves' disease, Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                 Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.067; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80227 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 3; 24pp; English.
                                                                                                                        14-JAN-2003; 2003WO-US001044
                                                                                                                                                                          14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||||||
1 LKAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                     Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-636703/60
                                                                                                                                                                                                                       (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                       WO2003060471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         saliva; ELISA.
                                                                    24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB80227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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ABB80227
X B X S X & & & & & & X B X B X B X S X X X X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) molety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                         LINF; lethal toxin neutralising factor; opossum; envenomation; therapy, anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.
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                                                                                                                           histamine reaction treatment
                                                                                                                                                                                                                                                                                                                             96US-00657163
                                                                                                                                                                                                                                                                                                                                                                               93US-00058387
                                                                                                                                                                                                                                                                                                                                                                                                      94US-00310340
N-terminus of opossum LTNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.3
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                          Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipps FW, Lipps BV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                                                                                                                                                                             03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                               10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1994;
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Gaps

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WO2003060471-A2

Synthetic.

saliva; ELISA

ABB80222;

RESULT 7

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Synthetic

24-JUL-2003

patient.

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polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                               New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Enterococcus faecalis polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 5938; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #22881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG22890 standard; protein; 156 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                       Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002 (first entry)
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SE NPTPPLWV 92
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                                                                                                            2003-895394/82.
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                                                       Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                      N-PSDB; ADH84648.
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(BUSH/) BUSH D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SXCCCCCCCCCCXXXXIIXXBXXIXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. aatchma, c.c. diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Relter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva cample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins from a sample assay of proteins from a sample as many a simple ELISA test, whereas an assay of proteins from a same and a simple ELISA test, whereas an assay of proteins from a same and a same a same and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                faecalis infection; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.5%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis polypeptide #2533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH88053 standard; protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 4; 24pp; English.
                                                    14-JAN-2003; 2003WO-US001044
                                                                                                         14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00134000,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                       WPI; 2003-636703/60
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                             (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial
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09-SEP-2003

ADH88053;

RESULT 9 ADH88053

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Length 137; 0; Indels

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MPO at the printed application.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 4; Length 156;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #18135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG18144 standard; protein; 303 AA.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 156 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed center of the second of the se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 303 AA;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (19E), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematocaus (SLEE), rheumatodia chapters, Siogran's syndrome, Reliev's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for sample using an anti-serum that is specific for the protein. Saliva collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas how a proteins from the assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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J, Zhang J, Ren F, Chen R, Wang ZW;
Goodrich R;
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein SEQ ID NO 3430.
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20-JUN-2000; 2000US-00598075.
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15-SEP-2000; 2000US-00653551.
15-CCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
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            8 \pm 8 
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                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to oytokine, call proliferation or cell differentiation or which may induce production of other cytokines in other cell propulations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SDO ID NO 2110 (AAK52581), 2111 (AAK52882) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a diterpene or diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                      Length 393;
                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 4; I
Pred. No. 1.5e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 220; 38pp; English
Claim 20; Page 332; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM98800 standard; protein; 932 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMG-CoA reductase polypeptide #53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus purpuratus
                                                                                                                                                                                                                                                                                                                                                      62.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-2002; 2002US-00041018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2001; 2001US-0259880P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 54.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 IKLLSPLPPLW 21
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKAMDPTPPLW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsuda SPT, Hart EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MATS/) MATSUDA S P T.
(HART/) HART E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-373921/35.
                                                                                                                                                                                                                                                                                                                  Sequence 393 AA;
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Gaps

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                                       conditions where the expression is induced, filtering the cell/resin mixture, extracting the cell/resin mixture, extracting the cell/resin mixture with alcohol to produce an organic eluent and analysing the organic eluent by a screening method including chromatography and/or spectroscopy, to identify the nucleic microorganism is useful as a diterpene synthase. The unicellular microorganism is useful as a diterpene or diterpene precursor producing system. Diterpenes, in plants, serve as defence toxins, volatile defensive signals, pollinator attractants and photoprotectants. This sequence represents an info-oA reducease polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein associated factor; dTAFISO; screening; diagnostic; gene transcription regulation.
             acid sequence of a yeast expression library, and the expression of the nucleic acid sequence is regulated by an inducible promoter under
 cells further comprises at least one isolated and purified nucleic
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                             Score 43; DB 8; Length 932;
Pred. No. 3.4e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATA-binding protein-associated factor dTAFI50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Arg, Pro or His"
                                                                                                                                                                                                       USPTO at segdata uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR56496 standard; protein; 1189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Val or Leu"
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Weinzierl ROJ;
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1176
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                                                                                                                                                                                                                                                                62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                             Query Match 62.3
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                   298 ККІРРІМРІЙ 307
                                                                                                                                                                                                                                                                                                                        2 KAMDPTPPLW 11
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N-PSDB; AAQ70733.
                                                                                                                                                                                                                                     Sequence 932 AA;
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30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang E,
                                                                                                                                                                                                                                                                                                                                                                                                              AAR56496
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The TATA-binding protein associated factor hTAFISO (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating gene expression associated with human pathology. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                         Length 1189;
                                                                                                                                                                                                                                                                         Score 43; DB 2; Length 118
Pred. No. 4.4e+02;
1; Mismatches 3; Indels
                     Disclosure; Page 156; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 26, 2005, 18:36:56 Job time : 104.2 secs
                                                                                                                                                                                                                                                                           62.3%;
                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 66...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      589 LSAMDDSPVLWI 600
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                                                                                                                                                                                                                                    Sequence 1189 AA;
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Sequence 1, Appli
Sequence 1, Appli
Sequence 255201,
Sequence 255201,
Sequence 25702,
Sequence 205702,
Sequence 206702,
Sequence 220, Appli
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Sequence 220, Appli
Sequence 220, Appli
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                                                                May 26, 2005, 18:43:39; Search time 78.72 Seconds (without alignments) 52.587 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-047-945-4
US-10-047-945-5
US-10-047-945-5
US-10-047-945-1
US-10-047-945-1
US-10-047-945-1
US-10-424-599-151167
US-10-424-599-151167
US-10-424-599-151167
US-10-047-945-7
US-10-047-945-7
US-10-047-945-7
US-10-047-945-128480
US-10-177-293-228
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                              1462099 segs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                    1 LKAMDPTPPLWI 12
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                                                                                                              US-10-047-945-4
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Match Length
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72.3
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                                                                                                                           Perfect score:
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0044446664
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111
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Sequence 45321, A Sequence 3999, A Sequence 253125, Sequence 253126, Sequence 1220724, Sequence 133945, Sequence 133945, App Sequence 387, App
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 387,
Sequence 387,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
US-09-864-761-45321

US-10-424-599-173148

US-09-864-761-3999

US-10-424-599-253125

US-10-424-599-220724

US-10-424-599-179202

US-10-437-99-179202

US-10-097-065-274

US-10-0372-876-274
                                                                                                                                 US-09-989-722-387
US-09-989-722-387
US-09-989-727-387
US-09-989-731-387
US-09-991-732-387
US-09-991-163-387
US-09-991-163-387
US-09-991-163-387
US-09-993-604-387
US-09-993-604-387
US-09-992-598-387
US-09-992-598-387
US-09-991-181-387
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Corresponds to fragment 1-12 of 2 above
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                    Sequence 4, Application US/10047945
| Publication No. US20301575551
| GENERAL INFORMATION:
| APPLICANT: LIPPS, PREDERICK W. |
| APPLICANT: LIPPS, PREDERICK W. |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E ITLE OF INVENTION: (IGBLIMPLICATED DISORDERS FILE REFERENCE: FWLPATO15US CURRENT APPLICATION NUMBER: US/10/047,945 CURRENT PLILUG DATE: 2002-01-14 PRIOR APPLICATION NUMBER: |
| PRIOR APPLICATION NUMBER: |
| PRIOR PLILUG DATE: 2002-01-14 |
| PRIOR PLILUG DATE: |
| NUMBER OF SEQ ID NOS: 7 |
| SOFTWARE: WORDFERFECT 5.1 FOR WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 69; DB 14; Length 12; Best Local Similarity 100.0%; Pred. No. 0.00098; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic.
US-10-047-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKAMDPTPPLWI 12
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LENGTH: 12
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RESULT

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ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
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                   GENERAL INFORMATION:
APPLICANT: LIPPS, BINIB V.
APPLICANT: LIPPS, BINIB V.
TITLE OF INVENTION: DIGGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
FILE REFERENCE: FULPATIONSH US/10/047,945
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR PILLING DATE:
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
LENGTH: 10
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APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (19E) IMPLICATED
FILE REPERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
RIOR APPLICATION NUMBER:
PRIOR FILING DATE:
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100.0%; Pred. No. 1.3e+06;
tive 0; Mismatches 0;
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100.0%; Pred. No.
ative 0; Mismatcl
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// Publication No. US20040031072A1
// GENERAL INFORMATION:
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-047-945-6

Sequence 6, Application US/10047945

Publication No. US20030157555A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
OTHER INFORMATION: SYNTHESIZED.
OTHER INFORMATION: US 5,576,297.
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; OTHER INFORMATION: Synthetic.
US-10-047-945-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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US20030157555A1
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Best Local Similarity 100.
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Best Local Similarity luv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-047-945-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
            Sequence 2, Application US/10047945
Publication No. US20030157555A1
Publication No. US20030157555A1
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, PREDERICK W.
APPLICANT: LIPPS, PREDERICK W.
APPLICANT: LIPPS, PREDERICK W.
APPLICANT: LIPPS, PREDERICK W.
TITLE OF INVENTION: USEN OF U
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Publication No. US2003015755A1
Publication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, PREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOCLOBULIN FILE REPERENCE: FWLPATOLIUS
FILE REPERENCE: FWLPATOLIUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE:
PRIOR FILING DATE:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 69; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0: Indela
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100.0%; Pred. No. 0.0036;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: SYNTHESIZED. OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic. US-10-047-945-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 11; Conservative
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LENGTH: 15
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LENGTH: 11
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corresponds to fragment 1-8 of 2 above
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; Beblication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIB V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: IGES) IMPLICATED DISORDERS
; TITLE OF INVENTION: IGES) IMPLICATED DISORDERS
; FILE REFERRNCE: FWLPATOLISUS
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.3%; Score 43; DB 14; Length 8; 100.0%; Pred. No. 1.3e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indela
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US-10-424-599-205702
                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(144)
OTHER INFORMATION: unsure at all Xaa locations
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56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
Pred. No.
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.8%;
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US-10-047-945-7
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                                                                                                                                                       NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205702
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Glycine max
FEATURE:
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1 LKAMDPTP 8
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Best Local Similarity
Matches 8; Conserv
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us-10-047-94

APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Zhou Yihua
APPLICANT: Car Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBUCE: 38-21(3223)B
CURRENT PILLATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NOS: 285684
TYPF: LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151167, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 32-1(5323)B
CURRENT PILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 285684
SEQ ID NO 151167
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Zhou Yihuna
APPLICANT: Canou Yihuna
APPLICANT: Canou Yihuna
APPLICANT: Canou Yihuna
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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Pred. No. 42;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_107527C.1.pep
US-10-424-599-151167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
US-10-424-599-255201
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85.7%;
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Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Glycine max
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US-10-424-599-151167
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Length 82;

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APPLICANT: Sahin, Aysegual
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, THERAPY OF BREAST CANCER
TILLS REFERENCE: MR.-038
CURRENT APPLICATION NUMBER: US/10/17,293
CURRENT FILING DATE: 2002-06-21
PRIOR PELLING DATE: 2001-06-27
PRIOR PELLING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR PILING DATE: 2001-09-18
PRIOR PELLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR PILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
CONTACT OF THE CONTACT OF TH
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                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_30829C.1.pep US-10-437-963-128480
                                                                                                                                  Score 42; DB 16;
Pred. No. 66;
1; Mismatches 1
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US-09-864-761-45321
; Sequence 45321, Application US/09664761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 228, Application US/10177293
Publication No. US20030124128A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bast Jr., Robert C.
Hortobagyi, Gabriel N.
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, Xumei
Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
                                                                                                                                  Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative 1
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Best Local Similarity 77.8%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myer, Vic
Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MDPTPPLWI 12
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               FEATURE:
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
; APPLICANT: Earosa, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Bradzuk, Brad
; APPLICANT: Bradzuk, Brad
; APPLICANT: Di, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38 -21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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| Sequence 220, Application US/10041018
| Publication No. US20040072323A1
| GENERAL INFORMATION:
| APPLICANT: Matsuda, Selichi P.T.
| APPLICANT: Hart, Elizabeth A.
| TITLE OF INVENTION: Diterpne-Producing Unicellular Organism FILE REPERBNCE: POlogoUS1/10025547
| CURRENT APPLICATION NUMBER: US/10/041,018
| PRIOR APPLICATION NUMBER: US/10/041,018
| PRIOR APPLICATION NUMBER: US 60/259880
| RINGER OF SEQ ID NOS: 413
| SEQ ID NO 220
| SEQ ID NO 220
| LENGTH: 932
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                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_67316C.1.pep
US-10-437-963-168841
                                                                                                                                                                                                                                                                                                                                                                                                                  3.
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Pred. No. 71;
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 168841
LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                   63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 70.0
Matches : 7; Conservative
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298 KKIDPTMPLW 307
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ORGANISM: Oryza sativa
                                                                                                                                                                                              ORGANISM: Oryza sativa
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LENGTH: 82
                                                                                                                                                                                                                                 FEATURE:
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Gaps

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2; Indels

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FEATURE:
                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
OTHER INFORMATION: SWISSPROT HIT: O53951, EVALUE 6.40e+00
OTHER INFORMATION: EST_HUMAN HIT: A1986481.1, EVALUE 6.00e-16
US-09-864-761-45221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 54.5%; Score 41; DB 9; Length 37; Similarity 54.5%; Pred. No. 44; 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                    FILIER REFERENCE: AGANG EXPRESSION ANALYSIS BY MICROAL CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT PILING DATE: 2001-05-23

FRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/203,366

PRIOR PELICATION NUMBER: US 60/203,369

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00665

PRIOR PELICATION NUMBER: PCT/US01/00665

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00661

PRIOR PELICATION NUMBER: PCT/US01/00661

PRIOR PELICATION NUMBER: US 60/234,687

PRIOR PELICATION NUMBER: US 60/234,687
US20020048763A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
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2 KAMDPTPPLWI 12 |:| | | |: 5 KSMGPAPPRWM 15

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US-10-424-599-173148

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## Sequence 173148, Application US/10424599
## Publication No. US20040031072A1
## Publication No. US20040031072A1
### PublicANT: La Rosa Thomas J
### APPLICANT: Car You Withua
### TITLE OF INVENTION: Date: US03-04-28
### CURRENT APPLICATION NUMBER: US/10/424,599
### CURRENT APPLICATION NUMBER: US/10/424,599
### CURRENT APPLICATION NUMBER: US03-04-28
### CURRENT APPLICATION NUMBER: US03-04-38
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Sequence 2, Appli
Sequence 2, Appli
Sequence 5938, Ap
Sequence 13316, A
Sequence 20, Appl
Sequence 20, Appl
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Sequence 57545, A
Sequence 57265, A
Sequence 8760, Ap
Sequence 18, Appl
Sequence 4515, A
Sequence 42, Appl
Sequence 42, Appl
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444, App
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21988, A
41296, A
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-657-163A-1

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US-09-902-540-13316

US-08-188-582-20

US-08-188-582-20

US-08-270-767-43223

US-09-270-767-43223

US-09-270-767-45255

US-09-949-016-8760

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US-09-370-767-45215

US-09-370-767-444

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Maximum Match 100%
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seq length: 200000000
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Match Length
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SEQUENCE CHARACTERISTICS:
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Sequence 1, Application US/08657163A
Patent No. 574449

GENERAL INPORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYMTHETIC LITRES AND THEIR
TITLE OF INVENTION: UTLLITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITTLE OF THE VALUE OF SEQUENCES: 3
CORNETRY: USA
ZIPE TEXAS
COUNTRY: USA
ZIPE: 77401
COMPUTER: EMADABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: MS CONFATIBLE
OCHERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
CORPUTER: MS MORD 2.0
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/657,163A
FILING DATE: 12 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/310,340
FILING DATE: 10 MAX 1993
ATTORNEY/AGENT INFORMATION:
MAME: JOHN R. CASPERSON
RECISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: 22,561
TELEPHONE FERENCE TITLE THE MAY 1993
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: EMI-PAT-US-011
TELECOMMUNICATION NUMBER: FWL-PAT-US-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
AUTHORS: JOUANS PERALLES, ET AL.
TITLE: ANTI-SNAEVE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 69; DB 1; I
100.0%; Pred. No. 6.4e-05;
tive 0; Mismatches 0;
                DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE:
CELL IYPE:
CELL INE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
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INDIVIDUAL ISOLATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOHRNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL .
VOLUME: PROGRAMME AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 69; DB 1; 100.0%; Pred. No. 6.4e-05;
                 STRANDEDRESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORIGINAL WILD
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STRATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
                                                                                                                                                                                                                                                                                                                              ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
CLRARY:
CLONE:
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                           ADULT
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Best Local Similarity 100.
Matches 12; Conservative
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AMINO ACID
EDNESS: SINGLE
                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE:
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                                                                                                                                                                                                                                                                                 TISSUE TYPE: BLOOD CELL TYPE: CELL LINE:
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1 LKAMDPTPPLWI 12
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APPLICANT:
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Sequence 5938, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 032796-032

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 5938

LENGTH: 137
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Batent No. 683347
GENERAL INFORMATION:
APPLICANT: Gldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wisegand, Roger C.
APPLICANT: Wisegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof File Reference: 38-10(15849)B
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APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/ABGRI INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHFTICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecalis
US-09-134-000C-5938
                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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85 NPTPPLWV 92
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US-09-134-000C-5938
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                                                                                                                                                                                                                                                              LENGTH:
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APPLICANT: Ruppert, Siegfried
APPLICANT: Timothy
APPLICANT: Timothy
APPLICANT: Timothy
APPLICANT: Timothy
APPLICANT: Timothy
APPLICANT: Timothy
APPLICANT: Wang, Edith
APPLICANT: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: Ambarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
CONTRY: USA
ZIP: 94111-4187
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Datastin Dalage #10 Varsion #1 25
                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                          Score 43; DB 4; Length 397;
Pred. No. 33;
1; Mismatches 2; Indele
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                          62.3%;
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                                                                                                                                                                      TYPE: PRT // OKGANISM: Myxococcus xanthus US-09-902-540-13316
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         369 MDPEPPRWV 377
                                                                                                                                                                                                                                                                                                                                                                           4 MDPTPPLWI 12
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RESULT 10
US-09-270-767-42265
Sequence 42265, Application US/09270767
Petent No. 6703491
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ORGANISM: Drosophila melanogaster
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      CURRENT FILING DATE: 1999-03-17
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Best Local Similarity 54.5%;
Matches 6; Conservative
                              NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43223
LENGTH: 253
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70 IKAVSPSPNLW 80
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                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Tjian, Robert
APPLICANT: Tjian, Robert
APPLICANT: Dynlact, Erian D.
APPLICANT: Dynlact, Erian D.
APPLICANT: Tanese, Nose
APPLICANT: Weinzierl Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NOCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NORMESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COMPUTER: Libr PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLOPS/MS-DOS
SOFTWARE: TEN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: TSPLICATION NUMBER: US/08/646,715
PILING DATE: 28-JAN-1994
FILING DATE: 28-JAN-1994
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
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Pred. No. 1.1e+02;
1; Mismatches 3; Indel8
                                                                                                                                                                            Sequence 20, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
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LENGTH: 1213 amino acids
TYPE: amino acid
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Best Local Similarity 66.77
Best Local 8; Conservative
620 LSAMDDSPVLWI 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 LSAMDDSPVLWI 631
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GENERAL INFORMATION:
APPLICANT Homburger et al.
APPLICANT Homburger et al.
TITLE ON INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 42265
LENGTH: 360
                                                                                                    Gaps
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                                                        Query Match 59.4%; Score 41; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 43; Astches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 4; Length 198;
Pred. No. 48;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.0%; Score 40; DB 4; Length 360; Best Local Similarity 54.5%; Pred. No. 91; Matches 6; Conservative 3; Mismatches 2; Indels
; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-43223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57545
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56.5%;
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Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: ||| |:|
134 KSDDPTNPIW 143
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82 LDGNPPLWI 90
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US-07-857-224B-42
                                                                                                                                                                                                                                                                                                                                    US-08-477-396A-18
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                                                                                                                                                                            JAPPLICANT: URBORATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASERQ for Windows Version 4.0

LENGTH: 72
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US-08-477-396A-18
US-08-477-396A-18
Sequence 18, Application US/08477396A
Patent No. 587235
GENERAL INFORMATION:
APPLICANT: Chen, Lan Bo
APPLICANT: Liu, Yuan
ITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
ITLE OF INVENTION: A SOLING SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABINEST: CHEN POST Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/477,396A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 4
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,488
FILING DATE: 29-0CT-1993
APPLICATION NUMBER: US 08/448,388
FILING DATE: 28-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12502
                                                                                                                         Sequence 8760, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
                     :||: |:| ||
70 IKAVSPSPNLW 80
1 LKAMDPTPPLW
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61 RTMDPTPP 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human
                                                                                                            US-09-949-016-8760
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RESULT 13
US-09-270-767-45215
US-09-270-767-45215
Sequence 45215, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 37326-094
CURRENT FILING DATE: 1999-03-17
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 45215
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hallaubstrasse 151
CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 4; Length 210;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
FILING DATE: 31-OCT-1994

ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346

REFERENCE/DOCKET NUMBER: DFCI-333BX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDENDESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45215
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US-09-902-540-16548

US-09-902-540-16548

Sequence 16548, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wieganch C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof TIER REFERENCE: 38-10(15849) B

CURRENT APPLICATION UNDER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR PLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

LENGTH: 557
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.1%; Score 38; DB 4; Length 557; Best Local Similarity 62.5%; Pred. No. 3e+02; Matches 5; Conservative 2; Mismatches 1; Indels
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFTCATION: 436
PRIOR APPLICATION DATA: none:
TELECOMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 262 2437
TELERAX: none
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 48
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUMB: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT / ORGANISM: Myxococcus xanthus US-09-902-540-16548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKAMDPTPPL 10
| | : | | | | |
31 LKVVDPTPEL 40
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Search completed: May 26, 2005, 19:08:40
Job time : 28.56 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

May 26, 2005, 18:26:23 ; Search time 12.64 Seconds (without alignments) 60.897 Million cell updates/sec

US-10-047-945-7 Title: Perfect score:

1 LKAMDPTP 8 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	38	88.4	792	~	T29187	hypothetical prote
7	35	81.4	237	~	A42013	ŝ
m		81.4	323	Н	TVMVF6	kinase
4	35	81.4	380	Н	TVFVMM	protein kinase (EC
S		81.4	602	Н	TVRTRR	kinase
9	35	81.4	647	Н	S00644	kinase
7		81.4	648	٦	TVHUF6	kinase
80	35	81.4	648	Н	TVRTRF	protein kinase raf
6	34	79.1	66	N	G64225	ribosomal protein
10	33	76.7	350	7	E87327	hypothetical prote
11	33	76.7	444	~	PD0001	protein-glutamine
12	33	76.7	638	Н	TVXLRF	protein kinase raf
13	33	76.7	691	Н	A29996	protein-glutamine
14	33	76.7	2717	N	A34203	DNA-binding protei
15	32	× 74.4	262	N	E64679	tryptophan synthas
16	32	74.4	408	~	AB3370	probable transport
17	32	74.4	416	•••	AF2070	hypothetical prote
18	32	74.4		N	A44302	protein-glutamine
19	32	74.4	620	• •	AG1598	internalin like pr
20	32	74.4	638	7	140725	2-isopropylmalate
21	32	74.4	680	N	JC5133	protein-glutamine
22	32	74.4			B39045	protein-glutamine
23	32	74.4	687	н	A39045	protein-glutamine
24	32	74.4	687	N	S19680	protein-glutamine
25	32	74.4	698	ч	A47203	protein-glutamine
56	32	74.4	771	~	B38252	
27	32	74.4	783	~	JH0329	granulocyte colony
28	32	74.4	863	N	C38252	granulocyte colony
29	31	72.1	142	~	AE1681	similar o transcri

180 2 T16668 253 2 T37152 276 2 UG5285 285 2 UG5284 333 2 T21569 333 2 T4569 345 2 S21094 348 2 UG54 348 2 UG54 375 2 A32827 376 2 C84769 371 2 T33287 431 2 T33287	hypothetical prote probable oxidoredu carbonyl reductase	carbonyl reductase catechol 1,2-dioxy hypothetical prote	probable glycohydr hypothetical prote alpha-2-HS-glycopr	countertrypin prec hypothetical prote fetuin precursor - probable fibrillin	conserved hypothet hypothetical prote hypothetical prote
0 6 9 6 7 8 8 9 8 9 8 9 8 9 8 9 8 9 9 9 9 9 9 9	T16668 T37152 JC5285	JC5284 JC6206 T21569	T36869 T49597 S21094	JC5431 G87706 A32827 C84769	A81717 T33287 T17332
	0 0 0	000	0 0 0 0	9250	814
	72.1	72.1 72.1 72.1	72.1	72.1	72.1 72.1 72.1
222 222 222 222 222 222 222 222 222 22	31	3333	5 5 5 5	3333	313
31 72.1.1 31 72.1.1	330 331 35	6 6 6 6 6 4 8	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	w 4 4 4 y O ∐ G	4 4 4 6 4 7

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A;Gene: CESP:C55C3.3
A;Map position: 4
A;Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:US3335; PIDN:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3 A;Experimental source: strain Bristol N2; clone C55C3
hypothetical protein C55G3.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T29187 R; Woessne, J.; Stellyes, L. Submitted to the EMBL Data Library, April 1996 A; Reference number: 220585 A; Reference number: 220585 A; A; Accession: T29187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-792 <WOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 88.4%; Score 38; DB 2; Best Local Similarity 87.5%; Pred. No. 11; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Genetics:
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133 LKPMDPTP 140 œ 1 LKAMDPTP

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alpha-1-B-glycoprotein - North American opossum (fragments)
C;Species: Didelphis virginiana, Didelphis mareupialis virginiana (North American opossu C;Species: Didelphis virginiana, Didelphis mareupialis virginiana (North American opossu C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
R;Catanese, J.J; Kress, L.F.
B;Cotanistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum A;Reference number: A42013; MUID:92118834; PMID:1731898

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-237 <CAT>
A;CSS-references: UNIPROT:Q28359; GB:J05356
C;Keywords: glycoprotein

Gaps ö Query Match 81.4%; Score 35; DB 2; Length 237; Best Local Similarity 87.5%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 1; Indels

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1 LKAMDPTP

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Gaps

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C;Superfamily: Kinase-related transforming protein, protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; polyprotein; serine/threonine-specific px Rp. 3-46/Domain: protein kinase homology KIN> P;88-96/Region: protein kinase ATP-binding motif P;88-96/Region: protein kinase ATP-binding motif P;108/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N/Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-re; Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C;Accession: B26126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: rat protein kinase raf; protein kinase homology
C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon;
E;301-57/Domain: protein kinase homology KIN>
F;309-317/Region: protein kinase homology motif
F;309-Active site: Lys #status predicted
F;453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predictr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase raf-1 (EC 2.7.1.-) - chicken
NyAlternate names: kinase-related transforming protein raf-1; mht/raf; protein kinase c-
C;Species: Gallus Gallus (chicken)
C;Date: 18-Oct-1989 #sequence revision 23-Aug-1996 #text_change 09-Jul-2004
C;Accession: S00644; I50380; I50381
R;Koenen, M.; Sippel, A.E.; Trachmann, C.; Bister, K.
Oncogene 2, 179-185, 1988
A;Title: Primary structure of the chicken c-mil protein: identification of domains share
A;Reference number: S00644; MUID:88217299; PMID:3285296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P05625; EMBL:X07017; NID:g63232; PIDN:CAA30069.1; PID:g63233: R;Flordellis, C.S.; Kan, N.C.; Lautenberger, J.A.; Samuel, K.P.; Garon, C.F.; Papas, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RjIshikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A;Title: Rat c-raf concogene activation by a rearrangement that produces a fused protein. A;Reference number: A26126; MUID:87172791; PMID:3550433
   A;Title: Nucleotide sequence of avian carcinoma virus MH2: two potential onc genes, A;Reference number: A21137; MUID:84221892; PMID:6328485
A;Accession: A21137
                                                                                                      A,Molecule type: DNA
A,Residues: 1-210, 'E', 212-230, 'E', 232-380 <KA2>
A,Cross-references: GB:K02082
C,Comment: This protein is translated as a gag-mht or gag-mil polyprotein.
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-602 <1SH>
A;Cross-references: GB:M15428; NID:g206546; PIDN:AAA42002.1; PID:g206547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein kinase (EC 2.7.1.37) raf
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A; Residues: 1-647 < KOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTP
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                                                                                                                                                                                                                                                                                             A; Gene: mht; mil
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NyAlternate names: kinase-related transforming protein mil (mht); mil proto-oncogene pro
C,Spedeis: avian myelocytomatosis virus MH2

NyAlternate names: kinase-related transforming protein mil (mht); mil proto-oncogene pro
C,Spedes: avian myelocytomatosis virus MH2

A,Note: host Gallus gallus (chicken)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A00639; B00638; A21137
R;Sutrave, P.; Bonner, T.I.; Rapp, U.R.; Jansen, H.W.; Patschinsky, T.; Bister, K.
Nature 309, 85-88, 1984
A;Title: Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine ret
A;Reference number: A00639
A;Molecule type: DNA
A;Residues: 1-380 «SUT>
A;Cross-references: UNIPROT: P00531; GB:K02082
A;Note: the authors translated the codon CAG for residue 58 as Gly
R;Kan, N.C.; Flordellis, C.S.; Mark, G.B.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A;Reference number: A00638; MUID: 84121298; PMID: 6320371
                                                                                                                                                                                                             rotein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611
Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: kinase-related transforming protein; protein kinase homology (Keywords: ATP), oncogene; phosphotransferase; serine/threonine-specific protein kinase; 32-238/Domain: protein kinase homology «KIN» (330-38/Region: protein kinase ATP-binding motif (50/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                 C;Date: 27-Nov-1985 #Sequence revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A00638; A38020
C;Accession: A00638; A38020
R;Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A;Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murin A;Reference number: A00638; MUID:84121298; PMID:6320371
A;Reference number: A00638; MUID:84121298; PMID:6320371
A;Residues: 1-323 cKAN>
A;Residues: 1-323 cKAN>
A;Residues: 1-323 cKAN>
A;Residues: 1-323 cKAN>
A;Residues: VIR.
Science 224, 288-289, 1984
A;Title: Primary structure of v-raf: relatedness to the src family of oncogenes.
A;Reference number: A38020; MUID:84172180; PMID:6324342
A;Rocession: A38020
A;Molecule type: DNA
A;Residues: 1-323 cMAR>
C;Comment: This protein is translated as a gag-raf polyprotein.
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R;Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 3000-3004, 1984
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                                                                                                                                                                                                                                                                                          Species: murine sarcoma virus 3611
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A;Molecule type: DNA
A;Residues: 1-210,'E',212-380 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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Best Local Similarity
Matches 6; Conserv
LKAMDTTP
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Gaps

have been studied kinase C and other kinases,

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A.Pescription: catalyzes the formation of specific peptidyl-threonine-phosphate and pept A.Pesthway: MAP kinase cascade
C.Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prof C.Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology «KIN»
F.139-184/Domain: protein kinase C zinc-binding repeat homology «KIN»
F.355-363/Region: protein kinase APP-binding motif
F.347-613/Domain: protein kinase APP-binding motif
F.355-363/Region: protein kinase APP-binding motif
F.355-363/Region: protein kinase APP-binding motif
F.355-81/Binding site: phosphate (Ser) (covalent) #status predicted
F.159,165,173,176/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
F.259/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status experiments
F.268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status experiments
F.358/Active site: Lys #status predicted
F.499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
A;Title: Identification of the major phosphorylation sites of the Raf-1 kinase. A;Reference number: A43089; MUID:93352516; PMID:8349614
A;Contents: annotation; phosphorylation sites
A;Note: expression is ubiquitous in mammalian tissues that have been studied
C;Comment: After phosphorylation and activation by protein kinase C and other k
                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3p25-3p25
A;Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3;
                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119546; OMIM:164760
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Note: the list of introns is incomplete C, Function:
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Attanen, H. W.; Bister, K.
Attanen, H. W.; Bister, M. W.; Attanen, M.; A
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NyAlternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
NyOntains: protein kinase (EC 2.7.1.37)
C; Species: Homo aspiens (man)
C; Species: Homo aspiens (man)
C; Species: Homo aspiens (man)
C; Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C; Species: Homo aspiens (man)
C; Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C; Accession: A00637; IS7580
A; FEDAMER, T.I.; Oppermann, H.; Seeburg, P.; Kerby, S.B.; Gunnell, M.A.; Young, A.C.; Rag Nucleic Acids Res. 14, 1009-1015, 1986
A; Title: The complete coding sequence of the human raf oncogene and the corresponding st A; Reference number: A00637; MUID:86120351; PMID:3003687
A; Molecule type: mRNA
A; Residues: 1.648 cBON1>
A; Molecule type: MID: SB.; Sutrave, P.; Gunnell, M.A.; Mark, G.; Rapp, U.R.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene. A; Title: Structure and biological activity of human homologs of the raf/mil oncogene. A; Title: Structure and biological activity of human homologs of the raf/mil oncogene. A; Stesidues: 228-239, L., 241-541, I', 543-648 cBON2>
A; Stesidues: 228-239, L., 241-541, I', 543-648 cBON2>
A; Stesidues: 228-239, L., 241-541, I', S43-648 cBON2>
A; Cross-references: GB:L00212; NID:g190837; PIDN:AAA60247.1; PID:g496091
R; Morrison, D.K.; Heidecker, G.; Rapp, U.R.; Copeland, T.D.
B; Biol. Chem. 268, 17309-17316, 1993
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                                      fitle: Analysis of the cellular proto-oncogene mht/raf: Relationship to the Reference number: 150380; MUID:86098644; PMID:3002017
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Pred. No. 36;
1; Mismatches 1; Indels
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protein kinase raf-1 (EC 2.7.1.-) - rat
N;Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
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Cross-references: UNIPROT:P11345; GB:M15427; NID:g206544; PIDN:AAA42001.1; PID:g206545
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A, Pathway: MAP kinase cascade
A, Note: expression is ubiquitous in mammalian tissues that have been studied
C, Superfamily: protein kinase A-raf; protein Kinase C zinc-binding repeat homology; prot
C, Keywords: AFP; autophosphorylation; phosphoprotein; phosphorransferase; prote-oncogene
F,139-184/Domain: protein kinase C zinc-binding repeat homology «KZN»
F,355-363/Region: protein kinase APP-binding motif
F,347-613/Domain: protein kinase APP-binding motif
F,355-363/Region: protein kinase APP-binding motif
F,355/Reinding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F,259/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
F,357/Active site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F,399/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F,499/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
F,499/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
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                                          Length 648
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Pred. No. 36;
                                  Score 35; DB 1
Pred. No. 36;
1; Mismatches
DB .
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05:58:12 2005

Tue May 31

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A; Cross-references: UNIPROT: Q7M0F8
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Matches 5, Conservative
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167 VQALDPTP 174
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Matches 6; Conserr
                                                                                                                                                                    A;Residues: 1-444 <IKU>
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                                                                                                                    A; Status: preliminary A; Molecule type: mRNA
                                                                                                 A; Accession: PD0001
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A; Title: The minimal gene complement of Mycoplasma genitalium.
A; Reference number: A64205
A; Reference number: A64205
A; Reference number: A64205
A; Mulceule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-99 < TIGR>
A; Residues: 1-99 < TIGR>
A; Residues: 1-99 < TIGR>
A; Residues: Code: SCG3
C; Genetics: Code: SCG3
C; Superfamily: hypothetical protein ysxB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Caulobacter crescentus
Cispecies: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
CiAccession: B8737.
Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Erndlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-350 <STO>
A,Cross-references: UNIPROT:Q9AAG8; GB:AE005673; NID:g13421843; PIDN:AAK22617.1; GSPDB:G
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Species: Mycoplasma genitalium
| Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
| Accession: G64225
  Gaps
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  Indels
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  Mismatches
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  Conservative
                                                                        377 LKVVDPTP 384
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60 LKLIDPTP 67
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LKALTPTP 22
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Best Local Similarity
Matches 6; Conserv
                                            1 LKAMDPTP
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protein kinase raf-1 (EC 2.7.1.-) - African clawed frog
NALernate names: Kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: 801930; ISI254
R;le Guellec, R.; Paris, J.; Philippe, M.
Nucleic Acids Res. 16, 10357, 1988
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A; Residues: 1-638 < LEG>
A; Residues: 1-638 < LEG>
A; Cross-references: UNIPROT:P09560; EMBL:X12948; NID:g65027; PIDN:CAA31407.1; PID:g65028|
R; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Paris, J.; Le Fur, N.; Philippe, M.
Biol. Cell 72, 39-45, 1991
A; Title: Xenopus c-raf proto-oncogene: cloning and expression during oogenesis and early
A; Reference number: 151254; MUID:92096753; PMID:1721855
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C since cascad
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A;Cross-references: GB:S74063; NID:g241259; PIDN:AAB20707.1; PID:g241260
R;Ikura, K.; Nasu, T.; Yokota, H.; Sasaki, R.; Chiba, H.
Agric. Biol. Chem. 51, 957-961, 1987
A;Title: Cloning of cDNA coding for guinea pig liver transglutaminase.
A;Reference number: PD0001
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C;Keywords: aminoacyltransferase
F;89/Active site: Cys #status predicted
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 61;
3; Mismatches
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Gaps ö

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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUD:97394467; PMID:9252185

A;Accession: E64679

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-262 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P56141; GB:AE000632; GB:AE000511; NID:92314443; PIDN:AAD0832
C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
F;17-244/Domain: tryptophan synthase alpha chain homology <TRPA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.4%; Score 32; DB 2; Length 262; Best Local Similarity 75.0%; Pred. No. 54; Matches 6; Conservative 0; Mismatches 2; Indels
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Job time : 14.64 secs
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                                                                                                                            protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Accession: A29996
R;Ikura, K.; Nasu, T.; Yokota, H.; Tsuchiya, Y.; Sasaki, R.; Chiba, H.
Biochemistry 27, 2898-2905, 1988
A;Title: Amino acid sequence of guinea pig liver transglutaminase from its cDNA sequence A;Reference number: A2996; MUID:88294033; PMID:2900023
A;Accession: A2996
A;Molecule type: mRNA
A;Residues: 1-691 < IKUJ>
A;Cross-references: UNIPROT:P08587
A;Cross-references: UNIPROT:P08587
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Keywords: aminoacyltransferase
F;277/Active site: Cys #status predicted
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A; Accession: Proliminary
A; Residues: 1-277
A; Residues: A34779
A; Reference number: A34779
A; Reference number: A34779
A; Residues: Brotliminary; nucleic acid sequence not shown
A; Residues: 801-1072, N, 1074-1168, K', 1170-1225, V', 1227-1434, N', 1436-1607, I', 1609-16
A; Csuperfamily: HIV-EP2 enhancer-binding protein
C; Reywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding protein PRDII-BF1 - human

NiAlternate names: major histocompatibility complex enhancer-binding protein 1

NiAlternate names: major histocompatibility complex enhancer-binding protein 1

Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

N;Reference number: A34203; MUID:90169514; PMID:2106471
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E64679
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Lyis Bade Blank (nsbja)

us-10-047-945-7.open.rup

protein search, using sw model 1 OM protein

May 26, 2005, 18:18:07 ; Search time 61.12 Seconds (without alignments) 67.026 Million cell updates/sec Run on:

US-10-047-945-7

1 LKAMDPTP 8 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Q9tr78 didelphis m	Q8hz75 didelphis m		_		O19055 papio hamad		_	P00532 murine sarc	Q85453 murine sarc	Q67624 ic4 retrovi	P00531 avian retro	Q15278 homo sapien	Q99n58 mus musculu		P05625 gallus gall				P47475 mycoplasma			091902 rupestris s		Q758i7 ashbya goss			vibrio p	Q43221 triticum ae	Q9rj27 streptomyce	Q8p816 xanthomonas
ΩI	Q9TR78	Q8HZ75	DM43 DIDMR	Q8HZ74	900560	019055	Q9CU36	Q8HYX5	RAF MSV36	Q85 <u>4</u> 53	Q67624	MIL AVIMH	Q15 <u>2</u> 78	Q99N58	085632	RAF1_CHICK	RAF1 HUMAN	RAF1_MOUSE	RAF1 RAT	Y233 MYCGE	Q6CS47	091725	091902	0902Н8	075817	Q7S1F7	O90WGO	Q87NP1	043221	Q9RJ27	Q8P816
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& Query Match I	.100.0	100.0	100.0	100.0		-	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	79.1	79.1	79.1	79.1	79.1	ð	σ	76.7	9	9	76.7	76.7
Score	43	43	43	43	38	35	35	35	35	35	35	35	35	35	35	35	32	32	35	34	34	34	34	34	34	34	33	33	33	33	33
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08pjg8 08zyf6 081kf6 09deb2 09y3g7 09y3g7 09y3g8 09y112 091112 06h70 0813n0 0813n0	RESULT 1  OSTR78  AC 09TR78  AC 09TR78  D 10-MAY-2000 (TEMBLrel. 13, Created)  DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  S Didelphis marsupialis (Southern opossum)  OC Mammalia, Metatheria, Didelphimorphia; Didelphidae; Didelphis.  OC Mammalia, Metatheria, Didelphimorphia; Didelphidae; Didelphis.  NOTH TAXID=9268;  RN 11  RP SEQUENCE  RX MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;  RY Franse 40. Mouseatche H., Marangoni S., Oliveita B., Domont G.B.;  RT from the serum of South American Didelphidae.";  RT from the serum of South American Didelphidae.";  RT from the serum of South American Didelphidae.";  RI Toxicon 32:1237-1249(1994).  SQ SEQUENCE 17 AA; 1947 MW; CES5FB40E73B2A2A CRC64;  Rest Local Similarity 100.0%; Score 43; DB 2; Length 17;  Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0,	LKAMDPTP 8
Q8PJG8 PCN2_PYRAE Q8LKF6 Q9DEB2 Q8Y3G7 Q8Y3G7 Q9N3Z4 Q9AAG8 Q91T12 Q7MU18 Q63U18 Q61J19 Q61JF3 Q6HJF9 ALIGNWENTS	Created) Last seque Last seque Last seque On SUBUINT hern opossu a; Craniate phimorphia; 46694; DOI= Ascargizatio rican Didel CB55FB40E CB55FB40E ; Score 43;	Created) Last seque Last seque Last annot 1-D (Fragme niana (Nort a) Craniata phimorphia, EMBL/GenBa
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209 259 2736 285 285 380 380 375 375 375 375 375	MINARY; BLrel. BELrel. Alis (Say. Choracter Fubwed autche Hartial South 249(1997) 1007	MINARY; MINARY; BErel. 23, C BErel. 26, L tein DVOP51- alis virgini a; Chordata; ria; Didelph (02) to the E AN06911.1; L L L L L L L L L L L L L L L L L L L
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Hypothetical protein C55C3.6.
Name=C55C3.6; ORFNames=C55C3.6;
Caenorhabditis elegans.
                                                                                                                                                                                     InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
Pfam, PR00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Submitted (SEP-2004)
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STRAIN-Bristol N2;
WormBase Consortium;
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                          Gaps
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28-FBB-2003 (Rel. 41, Last sequence update)
05-UTU-2004 (Rel. 44, Last annotation update)
Venom metalloproteinase inhibitor DM43.
Velos marsuplails (Southern opossum)
Didelphis marsuplails (Southern opossum)
Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
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-!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IPR007110; Ig-like.
InterPro; IPR011015; LEM_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1; Length 291; Pred. No. 2.5;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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19-like V-type 1.
19-like V-type 2.
19-like V-type 3.
Potential.
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100.08;
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                        8; Conservative
                                                                                                                                                                                                                  STANDARD;
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                                                                                         42 LKAMDPTP 49
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 AA;
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9268;
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                                                                                                                                                                      RESULT 3
DM43 DIDMR
                        Matches
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08HZ74
1D 08HZ
AC 08HZ
DT 01-M
DT 01-M
DT 01-M
DS 010-M
OS Dide
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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018 (1998).
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 2; Length 291;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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STRAIN=Bristol N2;
Woesene J., Stellyes L.;
"The sequence of C. elegans cosmid C55C3.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AXI310J1; AAN06912.1; -.
HSSP; Q8NHL6; 1GOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; Score 43; DB Similarity 100.0%; Pred. No. 2.5 8; Conservative 0; Mismatches
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MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
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-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AP006463; AAB63196.1; ---

R HSSP; PS4763; JJPA.

GO; GO:0004713; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0016749; F:protein exinase activity; IEA.

R GO; GO:0016749; F:protein amino acid phosphorylation; IEA.

R GO; GO:0016749; F:transferase activity; IEA.

R GO; GO:0016749; F:transferase activity; IEA.

R GO; GO:0016749; F:transferase.

InterPro; IPR001019; Kinase like.

InterPro; IPR001045; Tyr pkinase.

R InterPro; IPR001045; Tyr pkinase.

R Pfam; PF00069; Pkinase; 1.
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ت
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas (Hamadryas baboon).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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                                                                                                                                        2; Length 274;
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                                                                                                                                                                            1; Indels
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(SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                              11 protein.
274 Aa; 30019 MW; D7EAE6046588BDA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AA; 34230 MW; 3512983ADF5D1A3B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               01-7AN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
C-RAF homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0109; TYRKINASE.
Prodom; PD000001; Proc kinase; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE JT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 AA
                                                                                                                                    88.4%; Score 38; DB
87.5%; Pred. No. 24;
iive 0; Mismatches
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              Wormbase; WBGene0016956; C55C3.6. Wormpep; C55C3.6; CE29736. Hypothetical protein. SEQUENCE
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                                                                                                                      Query Match
Best Local Similarity 87.5'
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Matches 6; Conservative
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Submitted (SEP-2004) to EMBL; US3335; AAL27232
                                                                                                                                                                                                                                                            133 LKPMDPTP 140
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LKVVDPTP 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001
01-JUN-2001
01-MAR-2004
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Q9CU36
ID Q9CU;
AC Q9CU;
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DT 01-J1
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Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subfamily.
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Q85453;
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085453
1D 085455
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DT 01-NO
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R GO; GO:0005886; C:plasma membrane; TAS.

R GO; GO:0004572; F:protein binding; IPI.

R GO; GO:00047243; P:protein kinase activity; TAS.

R GO; GO:0007243; P:protein kinase activity; TAS.

R GO; GO:0007243; P:protein kinase cascade; TAS.

R InterPro; IPR001009; Kinase like.

R InterPro; IPR008271; Ser_thr_pkin_AS.

R Probom; PF00069; Pkinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

R PROSITE; PS001107; PROTEIN KINASE ST; 1.

R PROSITE; PS00118; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C., Domont G.B., Ho P.L., Perales J.;
Domont G.B., Ho P.L., Perales J.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY163806; AAN64698.1; -..
HSSP; P24071, 10VZ.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 314 venom metalloproteinase inhibitor DM43b 314 AA, 34604 MW, 69D55F54486D35A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR.2003 (TrEMBLrel. 23, Created)
1-MAR.2003 (TrEMBLrel. 23, Last aequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
Venom metalloproteinase inhibitor DM43b precursor.
Didelphis marsuplais (Southern opossum)
Eukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphis.
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                                                                                                                                                                                                                                                                                                                                           81.4%; Score 35; DB 2; Length 308; 75.0%; Pred. No. 1.1e+02; ive 1; Mismatches 1; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serinc-threonine-protein kinase transforming protein raf
(EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                    308 AA; 35058 MW; F87DD6ABE27600BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
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                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 LKVVDPTP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 LKAMDTTP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9268;
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P00532;
                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Query Match
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ID RAF M
AC P0053
DT 21-JU
DT 05-JU
DE Serin
DE 1C 2
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QBHXX5
AC QBHX
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Murine sarcoma virus 1611.
Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
NCBL_TaxID=11812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; P000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00119; PROTEIN KINASE DOM; 1.
PROSITE; PS00119; PROTEIN KINASE ST; 1.
ATP-binding; Oncogene; Polyprotein; Serine/threonine-protein kinase;
                                                                                                 [1] --
SEQUENCE FROM N.A.
MEDLINE-84121298; PubMed=6320371;
MANION.E. Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
"A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
and by murine sarcoma virus 3611.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyprotein. Selongs to the Ser/Thr protein kinase family. RAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- MISCELLANEOUS: This protein is synthesized as a Gag-Raf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDINE-64172180; PubMed=6324342;
MATK G.E., Rapp U.R.;
"Primary structure of v-raf: relatedness to the src family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (By similarity).
ATP (By similarity).
Stocon acceptor (By similarity)
52A5423A66E36E36ZR3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323
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Pred. No. 1.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
101-NAR-2004 (TrEMBLrel. 26, Last annotation update)
3611 raf gene. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; PS4763; 1JPA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
Pfam; PP00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; K01691; AAA46579.1; ALT_INIT.
PIR; A00638; TVMVF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 AA; 36883 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 224:285-289(1984)
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LKVVDPTP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
MEDLINE-84121298; PubMed=6320371;
Kan N.C., Flordellis C.S., Mark G.E.; Duesberg P.H., Papas T.S.;
"A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
NON TER
                                                                                ENBL; KO2084; AAA46576.1; -.

ENBL; KO2084; AAA46576.1; -.

HSSP; QQWJP4; BAATP

GO; GO:000554; F:ATP binding; IRA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004669; P:protein amino acid phosphorylation; IEA.

GO; GO:0016089; P:protein amino acid phosphorylation; IEA.

GO; GO:0019088; P:yrotein amino acid phosphorylation; IEA.

GO; GO:0019088; P:yrotal assembly; IEA.

GO; GO:0019088; P:yrotal assembly; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005524; F.ATP binding; IEA.
GO:0004674; F.protein serine/threonine kinase activity; IEA.
GO:0004713; F.protein-tyrosine kinase activity; IEA.
GO:0016740; F.transferase activity; IEA.
GO:0006468; P.protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                              Science 223:813-816(1984).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; K02084; AAA46576.1; -.
HSSP; Q9WJP4; 1BM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. K77528; CAS4718.1; -. HSSP, P54763; LJPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.4%; Score 35; DB 2; Length 359; 75.0%; Pred. No. 1.3e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 AA; 40935 MW; 5B6C615C5331570D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                           Probom; PD000001; Prot Kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA
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InterPro; IPR000719; Prot Kinsse.

InterPro; IPR001245; Prot kinsse.

InterPro; IPR001245; Tyr pkinsse.

Pfam; PF00069; Pkinsse: 1.
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NCBL_TaxID=36381;
                                                                                                                                                                                                                       InterPro; IPR003036; Gag_D30.
InterPro; IPR011009; Kinase like.
InterPro; IPR001019; Proc Kinase.
InterPro; IPR008916; Retrov capsid C.
InterPro; IPR00871; Ser thr pkin_AS.
Pfam; PP02093; Gag_D30; I.
Pfam; PF02095; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q67624;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 75.0
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LKVVDPTP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IC4 retrovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=6328485;
Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
"Nucleotide sequence of avian carcinoma virus Mi2: two potential onc
genes, one related to avian virus MC29 and the other related to murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: By Iteelf the v-Mil oncogene has only weak transforming capacity but it abolishes the growth factor requirements of avian macrophages transformed by other oncogenes.
-!- CATALYTIC ACTIVITY: A protein = ADP + a phosphoprotein.
-!- MISCELLANEOUS: This protein is synthesized as a Gag-Mht or Gag-Mil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-84121228; PubMed-6320371;
Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
"A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611.";
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine,threonine-protein kinase; Transferase.
SEQUENCE 375 AA; 42459 WW; 7FB38ESC5886EDD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyprotein.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sutrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,
                                                                                                                                      ·,
                                                                                              Length 375;
                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                            P00531;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Serine/threonine-protein kinase transforming protein mil
                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 2.7.1.37).
Names-V-MIL; Synonyms-V-MHT;
Avian retrovirus MH2.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 81:3000-3004(1984).
                                                                                              Score 35; DB 2; I
Pred. No. 1.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                              380 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine retroviral oncogene v-raf.";
Nature 309:85-88(1984).
                                                                                                                                                                                                                                                                                                              PRT;
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PIR; A00639; TVFVNM.
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InterPro; IPR000719; Prot kinase.
                                                                                              h 81.4%;
Similarity 75.0%;
6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 223:813-816(1984)
                                                                                                                                                                                                                                                                                                              STANDARD;
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105 LKVVDPTP 112
                                                                                                                                                                          1 LKAMDPTP 8
                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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1 LKAMDPTP 8
                             Query Match
Best Local Similarity
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SEQUENCE
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                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:Drotein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPRO01009; Kinase like.

R InterPro; IPRO01245; Tyr_pkinase.

R InterPro; IPRO01245; Tyr_pkinase.

R Pfam; PRO0109; Prot kinase; 1.

R PROSITE; PS00101; PROTEIN KINASE ATP; UNKNOWN 1.

R PROSITE; PS50011; PROTEIN KINASE DOW; 1.

R PROSITE; PS50011; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Pfam; PF00069; Pkinase; 1.
Prodom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Oncogene; Polyprotein; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOI. Cell. | Biol. 5:1400-1407(1985).

-1 - SIMILARITY: Belongs to the Ser/Thr protein kinase family.

R EMBL; L00212; AAA60247.1; -.

R EMBL; L00206; AAA60247.1; JOINED.

R EMBL; L00209; AAA60247.1; JOINED.

R EMBL; L00209; AAA60247.1; JOINED.

R EMBL; L00219; AAA60247.1; JOINED.

R EMBL; L00213; AAA60247.1; JOINED.

R PRR; S60341; S60341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                     Protein kinase.

ATP (By similarity).

ATP (By similarity).

Proton acceptor (By similarity).

G -> E (in Ref. 3).

6498695FB7EBEESD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1; Length 380;
Pred. No. 1.4e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                              81.4%;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75...
6; Conservative
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                                                                                                                                                                                                           341
96
108
201
211
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110 LKVVDPTP 117
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88
108
201
211
213
380 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                Transferase.
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CONFLICT
SEQUENCE
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NP BIND
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MEDLINE=21481893; PubMed=11597136; DOI=10.1006/geno.2001.6627;
Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.;
Phylogenetic conservation of the makorin-2 gene, encoding a multiple zinc-finger protein, antisense to the RAF1 proto-oncogene.";
Genomics 77:119-126(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASS! MAISS! THREA.

MAD; MGI:97847; Rafi.

MGD; MGI:97847; Rafi.

MGD; MGI:97847; Rafi.

MGD; MGI:97847; Rafi.

MGD; MGI:90005829; C:cytosol; TAS.

MGC; GO:0005829; C:cytosol; TAS.

MGC; GO:0005829; C:cytosol; TAS.

MGC; GO:00058215; F:protein binding: PII.

MGC; GO:0007219; P:protein kinase activity; TAS.

MGC; GO:0007219; DAG_PE-bind.

MICEPPO; IPRO00719; Prote Kinase acacade; TAS.

MICEPPO; IPRO00719; Prote Kinase.

MICEPPO; IPRO00719; Prote Kinase.

MICEPPO; IPRO00719; Prote Kinase.

MR InterPro; IPRO0061; Prote Kinase.

MR Pfam; Pro0130; C11; 1.

MR Pfam; Pro0130; PRI MASE.

MR Prod0130; C11; 1.

MR PROMO09; DAGPEDOMAIN.

MR PROSITE; PSO0109; C1; 1.

MR PROSITE; PSO0107; PROTEIN KINASE ATP; UNKNOWN_1.

MR PROSITE; PSO0108; RBD; 1.

MR PROSITE; PSO0107; PROTEIN KINASE ST; 1.

MR PROSITE; PSO0108; RBD; 1.

MR PROSITE; PSO0108; RBD; 1.

MR PROSITE; PSO0108; PROTEIN KINASE ST; 1.

MR PROSITE; PSO0109; RINASE ST; 1.

MR PROSITE; PSO0109; RINASE ST; 1.

MR PROSITE; PSO0109; RINASE ST; 1.
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSURE_Liver;
Doi M., Abe S.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB057655; BAB39748.1;
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HSSP; P11345; IRRB.
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Score 35; DB 2; Length 421;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein Kinsse raf 1 (Fragment).
Name-Raf!; Synonyms-CRAF;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.4%; Score 35; DB 2; I 75.0%; Pred. No. 1.9e+02; tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               495 AA
                                                                  1; Mismatches
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   81.4%;
75.0%;
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nes 6; Conservative
                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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150 LKVVDPTP 157
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AEGURENCE FROM N.A.

WEDLINE=84261423; PubMed=6086317;

MEDLINE=84261423; PubMed=6086317;

Adalibert F., de Dinechin S.D., Righi M., Stehelin D.;

Adalibert F., de Dinechin S.D., Righi M., Stehelin D.;

The second oncogene mil of avian retrovirus MH2 is related to the src gene family.";

EMBO J. 3133-1338 (1984).

REMEL; X00578; CAA25238.1; -.

REMEL; X00578; CAA25238.1; -.

RO; GO:0019012; C:virion; IEA.

GO; GO:0019012; C:virion; IEA.

GO; GO:0016032; P:viral life cycle; IEA.

GO; GO:0016032; P:viral life cycle; IEA.

RICEPRO; IPR000721; Gag_D44.

RICEPRO; IPR00109; Kinase_like.

RICEPRO; IPR001096; Rinase_like.

RICEPRO; IPR001091; Retrov_capsid_C.

PERM; PP00607; Gag_D24; 1.

REAT: Pr000065; PRINABSE.

REAT: PR000071; Gag_D24; 1.
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                                                                                                                                                                                                                       085632 PRELIMINARY; PRT; 506 AA.
0156532; Q85633;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Avian retrovirus MH2.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
(11)
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SEQUENCE 506 AA; 56266 MW; 0583CE415DC06F6C CRC64;
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Best Local Similarity 75.0
Matches 6; Conservative
367 LKVVDPTP 374
                                                                                                                                                   RESULT 15
08563
AC 08563
AC 08563
DE Gag p
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RA AVIAN
RX MEDLI
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Search completed: May 26, 2005, 18:43:27 Job time : 64.12 secs

|| :|||| 236 LKVVDPTP 243 1 LKAMDPTP 8

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Gaps ö 14 Lague Blank (uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model • OM protein Run on:

May 26, 2005, 18:17:22 ; Search time 68.8 Seconds (without alignments) 44.972 Million cell updates/sec

US-10-047-945-7

1 LKAMDPTP 8 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:*geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Desc	ABB80228 Syntheti	ABB80227 Synthetic	AAW53843 Aaw53843 N-terminu	ABB80222 Synthetic			AAW11575 N-termina	AAW53841 N-terminu		AAP81131 c-raf-rel	AAO02179 Aao02179 Human pol	AAY43943 Yeast	ADF18626 Adf18626 Protein	ABO62609 Klebsiell	ABU08102 Human	ABM82924 Human	AAR22560 Aar22560 Mouse	AAR22562 Aouse	AAR22563 Aouse		AAR22561 Aar22561 Mouse	AAR22559 Aar22559 Mouse	AAR98215 Human	AAW13107 . Aaw13107 Human	
DB	-	7	~	7	7	7	~	N	7	Н	4	7	7	7	9	8	7	N	7	~	~	~	~	~	
% Query Match Length DB	80	0	ព	10	11	12	15	15	15	29	94	267	344	405	615	615	648	648	648	648	648	648	648	648	
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	
Score	43	43	43	43	43	43	43	43	43	35	35	35	32	35	35	35	35	32	35	35	35	35	35	35	
7 2	н	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Aaw17047 Mutant mo	Aaw17044 Human c-r	Aawl7045 Mouse c-r	Aaw17046 Mutant mo	Aaw17049 Mutant mo	Aaw62220 Raf-1 pro	Aaw95611 Homo sapi	Aay08981 Human c-R	Aaw30668 Mutant mo	Aaw30666 Mutant mo	Aaw30669 Mutant mo	Aaw30664 Human c-r	Aaw30667 Mutant mo	Aaw30665 Mouse c-r	Aay94501 Human c-r	Aab42701 Human ORF	Aab08773 Amino aci	Aag67619 Amino aci	Aab70295 Human c-R	Aag67440 Amino aci	
AAW17047	AAW17044	AAW17045	AAW17046	AAW17049	AAW62220	AAW95611	AAY08981	AAW30668	AAW30666	AAW30669	AAW30664	AAW30667	AAW30665	AAY94501	AAB42701	AAB08773	AAG67619	AAB70295	AAG67440	
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648	648	648	648	648	648	648	648	648	648	648	648	648	648	648	648	648	648	648	648	
1.4	1.4	1.4	1.4	1.4	1.4	1.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	1.4	1.4	
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3.5	3	35	35	35	35		35				35		35					35		
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	,

## ALIGNMENTS

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; ABB80228 standard; peptide; 8 AA. (first entry) Synthetic LINF, LT-8. saliva; ELISA. 06-NOV-2003 ABB80228; 

Synthetic.

WO2003060471-A2

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugetion to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA

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Gaps

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Length 9; 0; Indels

100.0%; Score 43; DB 7; I 100.0%; Pred. No. 1.8e+06; iive 0; Mismatches 0;

8; Conservative

Matches

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Local Similarity

Query Match

Sequence 9 AA;

888888888

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LKAMDPTP LKAMDPTP

AAW53843 standard; peptide; 10 AA.

AAW53843

N-terminus of opossum LINF

(first entry)

08-JUL-1998

AAW53843;

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arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; dlabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        ;
                                                                                                                                                                              Length 8;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                             ; Score 43; DB 7; L; Pred. No. 1.8e+06; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              ABB80227 standard; peptide; 9 AA
                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-2002; 2002US-00047945.
                                                                                                                                                               Query Match
Best Local Similarity 100.00
Best Local Similarity 100.00
                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic LINF, LT-9
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                                                                                                                                                   Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                  RESULT 2
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This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Elapidee, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Col 11; 11pp; English.
                                                                                                                                                                   histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                         93US-00058387.
                                                                                                                                                                                                                                                                                                         96US-00657163
                                                                                                                                                                                                     Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-271108/24.
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(LIPP/) LIPPS
                                                                                                                                                                                                                                                                                                         03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                         10-MAY-1993;
22-SEP-1994;
                                                                                                                                                                                                                                       US5744449-A.
                                                                                                                                                                                                                                                                         28-APR-1998.
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Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a

WPI; 2003-636703/60.

Claim 7; Page 4; 24pp; English.

patient,

The sequences given in ABB8022-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, seliter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, arthritis, Sjogren's syndrome, Reiter's syndrome, The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of the protein is relatively non-invasive when compared to blood collection is relatively non-invasive when compared to blood requires
                                                                                                                                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clotting time before centrifugation to separate serum. Saliva proteins
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                  100.0%; Score 43; DB 2; Length 10; 100.0%; Pred. No. 0.16;
                                                       0; Indels
                                                       Mismatches
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                                                                                                                                                                                                                ABB80222 standard; peptide; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                      (first entry)
                                                       Conservative
                                                                                                                                                                                                                                                                                                                            Synthetic LTNF, LT-10
Query Match
Best Local Similarity
8; Conserv?
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LIPPS F W.
                                                                                                         LKAMDPTP
                                                                                         1 LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    saliva; ELISA.
                                                                                                                                                                                                                                                                                      06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                     ABB80222;
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                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                 ABB80222
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invesive when compared to blood collection of serum. Saliva can be centrifuged immediately, whereas blood requires
                                                                                                                                                                                                                                                                   Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                         ABB80226 standard; peptide; 11 AA.
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                                                                                                                                                                                              06-NOV-2003 (first entry)
                                                                                                                                                                                                                                    Synthetic LTNF, LT-11.
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Best Local Similarity
Local 8; Conserve
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                        1 LKAMDPTP
LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003060471-A2.
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                                                                                                                                                                                                                                                                                                                                                               saliva; ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Gaps

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100.0%; Score 43; DB 7; Length 10; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Indels

8; Conservative

Query Match Best Local Similarity Matches 8; Conserv

100.0%; Score 43; DB 7; Length 11; 100.0%; Pred. No. 0.18;

RESULT 7

LKAMDPTP

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (MCF), insulin, myoglobin and/or adenosine deaminase (ADA). In Quarticular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, arthritis, Sjogren's syndrome, Reliter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva can be centrifuged immediately, whereas blood collection collection is essent. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifuged immediately, whereas blood requires contents as a simple ELISA test, whereas an assay of proteins from the contents of the protein strome contents and a sasay of proteins from the contents of the c
                                                                                                                                                                                                                                                                    Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 7; Length 12;
Pred. No. 0.2;
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                                                        ABB80225 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 4; 24pp; English.
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Similarity 100.0%;
8; Conservative 0;
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                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                Synthetic LTNF, LT-12.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                    06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                 ABB80225;
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RESULT (ABB8022)
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The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the liner peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
                                                                                                                                                                                                                                                                                                                              Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
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                                                                                                                                                                                                                                                               N-terminal peptide from lethal toxin neutralising factor.
                               AAW11575 standard, peptide; 15 AA.
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                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipps FW, Lipps BV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1994;
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                                                                                                                                                                25-MAR-2003
20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5576297-A
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                                                                                                 AAW11575;
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AAW11575
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WW.W.XEXEXEXEX
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (ITMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgB levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                     Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 43; DB 7; Length 15; 100.0%; Pred. No. 0.25; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oncogene related peptide; c-raf-related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c-raf-related peptide c-raf-1 (142-170)
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                                                                                                                                                                                                                                                                                                           Claim 3; Page 3; 24pp; English
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                     14-JAN-2002; 2002US-00047945
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                                                                                                                       Lipps BV, Lipps FW;
                                                                                                                                                              WPI; 2003-636703/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YANA/) YANAIHARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LKAMDPTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conserv
                                                         (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3P253325-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP81131;
                                                                                                                                                                                                                                                                     patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP8113
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogran's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depresaion;
                                                                                                                                                                                                                                                                                                                                                                                           - can neutralise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 43; DB 2; Length 15; 100.0%; Pred. No. 0.25; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Lethal Toxin Neutralising Factor peptide from opossum venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80223 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2003; 2003WO-US001044.
                                                                                                                                         96US-00657163,
                                                                                                                                                                               93US-00058387.
                                                                                                                                                                                                  94US-00310340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic LTNF, LT-15.
              Didelphis virginiana.
                                                                                                                                                                                                                                                                                                         Lipps BV;
                                                                                                                                                                                                                                                                                                                                                WPI; 1998-271108/24.
                                                                                                                                                                                                                                         LIPPS B V.
LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003060471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                         (LIPP/) LIPPS
(LIPP/) LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baliva; ELISA
                                                                                                                                         03-JUN-1996;
                                                                                                                                                                               10-MAY-1993;
                                                                                                                                                                                                     22-SEP-1994;
                                                       US5744449-A.
                                                                                                28-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2003
                                                                                                                                                                                                                                                                                                       Lipps FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches
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RESULT 9

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1; Indels Length

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Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
inflammation. Note: The sequence data for this patent did not i
of the printed specification, but was obtained in electronic fo
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; I
Pred. No. 1.8e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Predicting the folded structure of proteins.
                                                                                                     Score 35; DB 4
Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 225-228; 113pp; English.
                                                                                                                                                                                                                                                                                              AAY43943 standard; protein; 267 AA.
                                                                                                       81.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00857224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00857224
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Yeast protein kinase #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                         6; Conservative
                                                                                                                                                                                                            22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                          Local Similarity
                                                                                                                                                                                              ||: ||||
48 LKSQDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LKAMDPTP
                                                                                                                                                                          1 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 267 AA;
                                                                        Sequence 94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BENN/) BENNER
                                                                                                                                                                                                                                                                                                                                                                21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5958784-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benner SA;
                                                                                                                                                                                                                                                                                                                              AAY43943;
                                                                                                        Query Match
                                                                                                                                          Matches
                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                            AAY43943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynpeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                         solid phase or soln. methods. One of 3 c-raf-1-related peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; architits; inflammation.
                                                                   New oncogene related peptide(s) - useful in prepn. of antigen and then antibodies having specific reactivity with cancer proteins.
                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                       among 23 claimed oncogene-related peptides. See also AAP81114-30 an AAP81132-P81134. (Updated on 01-JUL-2002 to add missing PI field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 16071; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                              81.4%; Score 35; DB 1; Length 29; 75.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 16071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA002179 standard; protein; 94 AA.
                                                                                                                        Claim 19; Page 33; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126,
18-MAY-2000; 2000US-00577409,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                6; Conservative
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LKVVDPTP 16
     Yanaihara N;
                                                                                                                                                                                                                                                                                                                                                  8
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                                     WPI; 1988-015700/03
                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                1 LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI82110.
                                                                                                                                                                                                                                              Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO02179;
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                                                                                                                                                          Prepd by
                                                                                                                                                                                                                                                                              Query Match
     Abe K,
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Length 267; 1; Indels

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Klebsiella pneumoniae protein; antibacterial; Vaccine.
                       Klebsiella pneumoniae
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186 IKARDPTP 193
                                                                                                                                                                            WPI; 2003-895346/82
                                                                                                                                                                                                                                                                                                                                                                                                                       1 LKAMDPTP 8
                                                                                                                                                                                       N-PSDB; ACH96160
                                                                                                                                                                                                                                                                                                                                                        Sequence 405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402003012065-A2
                                                                                                            29-JAN-1999;
                                            US6610836-B1
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                                                                                                                                                       Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU08102;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of protein c-Raf-1 (amino acids 305-648). Human papillomavirus oncoprotein E7 abrogates Raf-associated arrest and prevents inhibition of cyclin E-CDK2 activity without disrupting Raf induction of p21Cip21. E7 neither interacts with p21Cip1 nor derepresses p21Cip1-associated CDK2 activity, but instead reduces the association between p21Cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-state levels of Akt, a regulator of p21Cip1 localisation, leading to loss of p21Cip1 phosphorylation and accumulation of p21Cip1. E7 disrupts the effects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation. Maintenance of Akt activity is necessary and sufficient to bypass Raf arrest. The invention provides methods for identifying and using compounds capable of promoting the nuclear localization of p21Cip1. The methods can be used to inhibit aberrant cellular proliferation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                          Identifying a compound that inhibits B7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                           Human; c-Raf-1; oncoprotein E7; p21CIP1; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant expression vector; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 7; Length 344;
Pred. No. 2.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella pneumoniae polypeptide seqid 9126.
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 2; 119pp; English.
                     ADF18626 standard; protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO62609 standard, protein, 405 AA
                                                                                                                                                                                                                      19-APR-2002; 2002US-0374245P.
                                                                                                                                                                                                21-APR-2003; 2003WO-US012667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.08;
                                                                                      Protein c-Raf-1 (aa305-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                Mccance D, Westbrook TF;
                                                                                                                                                                                                                                          (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :||||
LKVVDPTP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LKAMDPTP 8
                                                                                                                                                                                                                                                                                      WPI; 2003-845498/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 344 AA;
                                                                                                                                                     WO2003088922-A2.
                                                                                                                                Homo sapiens
                                                                12-FEB-2004
                                                                                                                                                                          30-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-2004
                                           ADF18626;
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                                                                                                                                                                                                                                                                                                                                             activity
RESULT 13
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ID ABO6
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KW Recx
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New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a new isolated nucleic acid encoding a Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; enzyme; kinase and phosphatase; KPP; cancer; cirrhosis; cell proliferative disorder; arteriosclerosis; atherosclerosis; hepatitis; parcoxyman inocturnal haemoglobinuria; polycythaemia vera; psoriasis; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anemaia mental retardation; AIDS; epilepsy; neurological disorder; Alzheimer's disease; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; asthma; acquired immunodeficiency syndrome, autoimmune thyroiditis; contact dermatitis; Crohn's disease; diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout; Graves' disease; glomerulonephritis; Goodpasture's syndrome; multiple sclerosis; osteoprosals; pancreatitis; Reiter's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis; infection.
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Pred. No. 2.8e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 9126; 932pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU08102 standard; protein; 615 AA.
                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.4%;
27-JAN-2000; 2000US-00489039.
                                                                                  99US-0117747P.
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nes 6; Conservative
                                                                                                                                                                                                                                                        Osborne M;
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01-AUG-2002; 2002WO-US024521
                                                                 Sequence 615 AA;
  02-AUG-2001;
   07-AUG-2001;
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ö Gaps ö 81.4%; Score 35; DB 6; Length 615; 75.0%; Pred. No. 4.4e+02; 1; Indels 1; Mismatches 6, Conservative 1 LKAMDPTP 8 Query Match Best Local Similarity Matches 6; Conserv ð

344 LKVVDPTP 351

Search completed: May 26, 2005, 18:36:58 Job time : 70.8 secs

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase, KPP (KPP-1 to KPP-18). Also included are the encoding polymucleotides KPP MA, recombinant polymucleotides (FPP-16). Also included are the encoding polymucleotides KPP MA, recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, an anti-KPP antibody, screening for anti-Agonists of KPP, microarray where at least one element is KPP NA, generating an expression profile of a sample containing comprised and an array comprising different nucleotide molecules or polymucleotide sequence specifically hybridisable with at least 30 affixed in distinct physical locations on a solid substrate (where at least one of the nucleotide molecules comprises a first oligomucleotide contiguous nucleotides of a target KPP NA). The kinases and phosphatases of polymucleotides or preventing discorders and phosphatases (KPP) polypeptides, polymucleotides, agonists and antagonists are useful for dispancing, retaining or preventing discorders (seq. Contiguous nucleotides, alternation or cancer), developmental disorders (real tubular expression of KPP, particularly cell proliferative disorders (e.g. thromobovytopeania or mencer), developmental disorders (real conternal nemmoglobinuria, polycythaemia vera, psoriasis, prinary thromobovytopeania or mencer). Alevelopmental disorders (e.g. Albeiner's disease, parkingon's disease or epilepsy), autoimmum autoimmum thyroiditis, contact demaritis, Craves' disease, parkingon's disease or epilepsy), autoimmum autoid arthritis, sogeren (sequences of proteins associated con the expression of nucleic acid and as sequences of proteins associated con the expression of nucleic acid and as sequences of proteins associated con the New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis. ίχ, He A, Au-Young JK, Lee SY; VS, Ison CH, Yang J, Lee EA, Li J) Warren BA, Hafalia AJA, Marquis JP; Claim 1; Page 159-160; 199pp; English. Baughn MR, Yue H, Walia NK, Gietzen KJ, Lal PG, Elliott Emerling BM, Richardson TW, 07-SEP-2001; 2001US-0317820P 14-SEP-2001; 2001US-0322264P 28-SEP-2001; 2001US-0326098P 19-DEC-2001; 2001US-0343007P 2001US-0310933P 2001US-0309627P 2002US-0364494P 24-APR-2002; 2002US-0375539P (INCY-) INCYTE GENOMICS INC. WPI; 2003-239519/23. N-PSDB; ABX13149.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                      May 26, 2005, 18:43:39 ; Search time 52.48 Seconds (without alignments) 52.587 Million cell updates/sec
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1. (egn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*

1. (egn2_6)ptodata/1/pubpaa/US06_NEW_PUB.pep:*

1. (egn2_6)ptodata/1/pubpaa/US06_PUBCOMB.pep:*

2. (egn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*

2. (egn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*

3. (egn2_6)ptodata/1/pubpaa/US08_NEW_PUB.pep:*

3. (egn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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3. (egn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3. (egn2_6)ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4. (egn2_6)ptodata/1/pubpaa/US09_PUBCOMB.pep:*

5. (egn2_6)ptodata/1/pubpaa/US09_PUBCOMB.pep:*

5. (egn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*

6. (egn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*

6. (egn2_6)ptodata/1/pubpaa/US10P_PUBCOMB.pep:*

6. (egn2_6)ptodata/1/pubpaa/US60_NEW_PUB.pep:*

6. (egn2_6)ptodata/1/pubpaa/US60_NEW_PUB.pep:*

6. (egn2_6)ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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Result

Sequence 13464, A Sequence 13616, A Sequence 13410, A Sequence 13410, A Sequence 13410, A Sequence 13410, A Sequence 13, Appli Sequence 3, Appli Sequence 4, Appli Sequence 490, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 12, Appli Sequence 131816, Sequence 131816, Sequence 13621, A Sequence 13622, A Sequence 13627, A Sequence 1362	
US-10-732-923-13464 US-110-732-923-13646 US-110-732-923-13646 US-110-732-923-13646 US-110-732-923-13646 US-110-732-923-13440 US-10-060-065-17 US-10-059-585-38 US-110-059-585-38 US-110-059-585-38 US-110-059-585-38 US-110-059-584-4 US-110-059-584-4 US-110-926-543-90 US-110-926-5122 US-110-926-5122 US-110-928-131815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-424-599-151815 US-10-434-675-6 US-110-732-923-13625 US-110-732-923-13625	ALIGNMENTS
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US-10-047-945-7

US-10-047-945-7

Sequence 7, Application US/10047945

Publication No. US20030157555A1

GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, BINIE V.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (JEB) IMPLICATED DISORDERS

TITLE OF INVENTION: UNMBER: US/10/047,945

CURRENT APPLICATION NUMBER: 2002-01-14

PRIOR PILING DATE: 2002-01-14

PRIOR FILING DATE: 7

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

ILENGTH: 8

TYPE: PRT

PRATURE: AMBERTER: 100.0%; SCOIM 43; DB 14; Length 8; Best Local Similarity 100.0%; Pred. No. 1.30+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

Overy Match

| HIMINITION | HIMADPTP 8

| LIKAMDPTP 8
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RESULT 2

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; Publication No. US2003015755A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (1991) IMPLICATED DISORDERS
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; RICK REPLICATION NUMBER:
; RICK REPLICATION NUMBER:
; RICK PLEING DATE: 1 FOR WINDOWS
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LIPPS, BILL

APPLICANT: LIPPS, BREBERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS

FILE REFRENCE: FWLPATOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 43; DB 14; Length 11; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic.
US-10-047-945-5
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 8; Conserv
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US-10-047-945-2
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US-10-047-945-4
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| Sequence 1, Application US/10047945 |
| Sequence 1, Application US/10047945 |
| Publication No. US200301575551 |
| GENERAL INPORMATION: |
| APPLICANT: LIPPS, BINIE V. |
| APPLICANT: LIPPS, FREDERICK W. |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E |
| TITLE OF INVENTION: (IgBl IMPLICATED DISORDERS |
| FILE REFERENCE: FWLPAT015US |
| CURRENT APPLICATION NUMBER: US/10/047,945 |
| PRIOR APPLICATION NUMBER: |
| PRIOR APPLICATION NUMBER: |
| PRIOR PILLING DATE: 2002-01-14 |
| PRIOR PILLING DATE: |
| PRIOR PILLING DA
                             Sequence 6, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION.
APPLICANT: LIPPS, BINIE V.
APPLICANTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E TITLE OF INVENTION: DISCORDERS
FILE REFERENCE: FWLDATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE:
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Pred. No. 0.16;
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Pred. No. 1.3e+06;
0; Mismatches 0;
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10047945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%;
Similarity 100.0%;
8; Conservative 0;
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Best Local Similarity 100.0%;
Matches 8; Conservative 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 8; Conserv
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US-10-047-945-5
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LENGTH: 9
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgetton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT APPLICATION NUMBER: 10/310,154
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PRILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
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                                                                                              81.4%; Score 35; DB 17; Length 323; 75.0%; Pred. No. 1.9e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BERMER, RYAN
APPLICANT: BERMER, RYAN
APPLICANT: KUMAR, ABHINAV
APPLICANT: KUMAR, ABHINAV
APPLICANT: MIBBIRN, MICHAEL V
APPLICANT: MIBBIRN, MICHAEL V
APPLICANT: MIBBIRN, MICHAEL V
TILLE OP INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR PILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE PARENTIN VET: 3,2
LENGTH: 350
       i TYPE: PRT

    ORGANISM: Murine sarcoma virus 3611
US-10-732-923-13460
                                                                                                                                                                                                                                                                                                                                                 Sequence 139, Application US/10664421; Publication No. US20040142864A1; GENERAL INFORMATION:
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Best Local Similarity 75.v.,
-hog 6; Conservative
                                                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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CRGANISM: Homo sapiens
US-10-664-421-139
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52 LKVVDPTP 59
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TYPE: PRT
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i Sequence 13683, Application US/10732923

i Publication No. US20050108791A1

i GENERAL INFORMATION.

I APPLICANT: Edgerton, Michael D

ITILE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REPERENCE: 38-15(52796)C

CURRENT APPLICATION NUMBER: 10/10/732,923

CURRENT FILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: 10/310,154

PRIOR PLING DATE: 2002-12-04

i NUMBER OF SEQ ID NOS: 24149

i SEQ ID NO 13683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13460, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION;
; APPLICANT: EGGETCON, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT FILING DATE: US/10/732,923
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13460
; LENGTH: 323
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN B
TITLE OP INVENTION: (192) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATO1SUS
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 2
LENGTH: 15
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 6; Conservative
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NAME/KEY:
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Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: THANSGENIC

FILE REFERENCE: 38-15(52796)C

CURRENT PELLING DATE: 2003-12-10

PRIOR FILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 13465

LENGTH: 380
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                                                                                                                               GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US,10/732,923
CURRENT PILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-04
PRIOR FILING DATE: 2002-12-04
SEQ ID NOS: 24149
SEQ ID NO 13529
LENGTH: 375
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REFREENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: 2003-12-10
PRIOR FILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13463
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 17; Length 375;
Pred. No. 2.2e+02;
1; Mismatches 1; Indels
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                                                                                             Sequence 13529, Application US/10732923
Publication No. US20050108791A1
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Best Local Similarity 75.0°
Matches 6; Conservative
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; ORGANISM: IC4 retrovirus
US-10-732-923-13529
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88 LKVVDPTP 95
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; Sequence 13646, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
   APPLICANT: Edgerton, Michael D
   TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REPERENCE: 38-15 (52796)
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; RIOR PLING DATE: 2003-12-04
; RIOR PLING DATE: 2002-12-04
; SEQ ID NO 13646
                                                                                                                                                                                                                             US-10-732-923-13464
; Sequence 13464, Application US/10732923
; Publication No. US2050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION:
; FILE REFERENCE: 38-15 (52796)
; CURRENT APPLICATION NUMBER: US/10/732, 923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13464
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                                                   Score 35; DB 17; Length 410;
Pred. No. 2.4e+02;
1; Mismatches 1; Indels
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Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
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; ORGANISM: Avian myelocytomatosis virus MH2
US-10-732-923-13464
ORGANISM: Avian myelocytomatosis virus MH2 US-10-732-923-13463
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                                                     81.4%;
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Best Local Similarity 75.0.
                                    Query Match
Best Local Similarity 75.0
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Best Local Similarity 75.0
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Gallus gallus
US-10-732-923-13646
                                                                                                                                             || :||||
140 LKVVDPTP 147
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140 LKVVDPTP 147
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140 LKVVDPTP 147
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                                                                                                                          1 LKAMDPTP 8
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STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID
HYPOTHETICAL: NO
ANTI-SENSE: NO
PRAGMENT TYPE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: SIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-657-163A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 42, Appli
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112, Appl
112, Appl
112, Appl
1126, Ap
1126, Ap
11, Appl
12, Appl
13, Appl
13, Appl
14, Appl
15, Appl
16, Appl
17, Appl
18, Appl
18, Appl
19, Appl
19, Appl
19, Appl
19, Appl
10, Appl
10, Appl
11, Appl
                                                                                                                                             May 26, 2005, 18:29:58; Search time 18.24 Seconds (without alignments) 32.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 12,
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Sequence 3
Sequence 4
Sequence 5
Sequence 1
Sequence 6
Sequence 6
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1: /cgn2_6/ptodaca1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodaca1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodaca1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodaca1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodaca1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodaca1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodaca1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-657-163A-2
US-08-310-340A-1
US-08-57-163A-4
US-08-57-163B-42
US-08-57-224B-42
US-08-909-984A-12
US-08-909-983-12
US-08-909-983-12
US-08-909-983-12
US-08-185-282-1
US-08-185-282-2
US-08-185-282-3
US-08-185-282-4
US-08-185-282-4
US-08-185-282-4
US-08-185-282-4
US-08-185-282-4
US-08-185-282-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-081-320-27
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                                                                                                                                                                                                                                                                                                                                                                                                                              513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                           US-10-047-945-7
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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Sequence 27, Appli
Sequence 5, Appli
Sequence 27, Appli
Sequence 140, App
Sequence 13211, A
Sequence 3760, Ap
Sequence 3760, Ap
Sequence 5555, Ap
Sequence 5255, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 10140, A
Sequence 10140, A
                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08657163A; Patent No. 574449; GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND TITLE OF INVENTION: SYNTHETIC LINES AND THEIR TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
US-09-707-780-27
US-09-568-189A-5
US-09-956-189A-27
US-09-602-540-13211
US-09-134-006-3881
US-09-134-006-3881
US-09-543-681A-5055
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-535
US-09-543-681A-6
PCT-US91-09784-4
PCT-US91-09784-4
US-09-949-016-10140
US-09-949-016-10140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER 1/40.1

COMPUTER TEADABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1 BM COMPATIBLE
OFBRATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION STARE: 08/310,340
FILING DATE: 10 MAY 1993
ATTORNEY AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
TELEROMMUNICATION NUMBER: FWL-PAT-US-011
TELEPAN: 713-462-2961
                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
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COUNTRY: USA
                   TITLE: AL
JOURNAL:
JOURNAL:
                                                                                                                                                                                          US-08-310-340A-1
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US-08-657-163A-1
                                                                       VOLUME:
VOLUME:
VOLUME:
ISSUE: E
 AUTHORS:
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PRICED IN STACE 1
CENERAL INFORMATION:
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
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0
                                                       100.0%; Score 43; DB 1; Length 10; 100.0%; Pred. No. 0.018;
                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM;
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE:
ORGAL LINE:
ORGALLIE:
ORGALE:
OMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION WHEER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-6845
TELEPAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: BLOOD
                                                                                                                                                           1 LKAMDPTP 8
                                                                                                                                     1 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAPLOTYPE:
       US-08-657-163A-2
                                                                                                                                                                                                                                                      US-08-310-340A-1
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Gaps
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APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 43; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 0.028; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                   10TH WORLD CONGRESS ON ANIMAL
PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
SINGAPORE
PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
SOFTWAREN: APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
: JONAS PERALES, ET AL.
ANTI-SYMBE VENOM FORM DIDELPHIDAE
.: INTERNATIONAL SOCIETY ON
.: TOXINOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NOMBER: 05/05/05/103
PILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
PILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAX 1993
ATYONEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: PWL-PAT-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: PROTEIN IN SEQ ID HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08657163A Patent No. 5744449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: BINIE V. LIPPS
4509 MIMOSA DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 713-482-296
TELEFAX: 713-663-7290
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                               DATE: 3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                              1 LKAMDPTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTP 8
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us-10-047-945-7.open.rai

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LENGTH: 315 amino acids
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                   31 LKVVDPTP 38
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44 LKVVDPTP 51
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STRANDEDNESS: no
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                      PAGES: 42-52
DATE: 1988
                                                                                                                                                           US-07-857-224B-42
                                                                                                                                                                                                                                                                                                                                                                                              US-08-571-758-12
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CUNTRY: Switzerland
ZIP: (note: this is an international post code)
ZIP: (note: this is an international post code)
ZIP: (note: this is an international post code)
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 03/25/92
CLASSIPICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INPORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
                                                                                                                                                                                         CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JUNTERNATIONAL. SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: TOXICOLOGY
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 43; DB 1; Length 15; 100.0%; Pred. No. 0.028; tive 0; Mismatches 0; Indels
                                                                                                                                    ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              υπωπΝΙΣΜ: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 48
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42, Application US/07857224B Patent No. 5958784
                      TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
STRAIN: WILD
INDIVIDUAL ISOLATE: 7
DEVELOPMENTAL STAGE:
                                                        HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                            3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-657-163A-1
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Patent No. 5700675
GENERAL INPORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Pelix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: A No. 5700675el Protein Kinase Required for Ras
TITLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                           Score 35; DB 2; Length 267; Pred. No. 28; 1; Mismatches 1; Indels
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Pred. No. 34;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: SEB BUGH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%; Score 35; 75.0%; Pred. No. 3
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           n 81.4%;
Similarity 75.0%;
6; Conservative 1
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TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
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us-10-047-945-7.open.rai

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44 LKVVDPTP 51
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Best Local Similarity
Matches 6; Conserv
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US-08-276-151-5
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Sequence 12, Application US/08909983

Sequence 12, Application US/08909983

GENERAL INFORMATION:

APPLICANT: Rubin, Gerry M.

APPLICANT: Chang, Henry C.

APPLICANT: Karim, Felix D.

APPLICANT: Wassarman, David A.

TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras

TITLE OF INVENTION: Signal Transduction

NUMBER OF SEQUENCE: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE TECHNOLOGY LAW GROUP
       Sequence 12, Application US/08909984A

Patent No. 5747275

GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Karim, Felix D.
APPLICANT: Wassarman, David A.
ITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras TITLE OF INVENTION: Signal Transduction
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,984A
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-4
TELECPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
TELEPK: (415) 343-4341
TELEFK: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 315 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPANDEDNESS: not relevant
MOLECULE TYPE: peptide
US-08-909-984A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 268 BUSH STRI
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 LKVVDPTP 51
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US-08-909-984A-12
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WENTING TYPE: 100 POWERS

WENTING TYPE: 100 POWERS

WENTING TYPE: 100 POWERS

WENTING TYPE: 100 POWERS

WENTING SYSTEM: 100 POWERS

WENTING WENTING WASHER

TELEVING WENTING WASHER

WATCHARD ADDRESS

MATCHARD ADDRESS

TELEVING WASHER

MATCHARD ADDRESS

MATCHARD ADD
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Gaps
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                                                                                                                                                                                                                                                                                 Length 648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rapp, U1f R.
APPLICANT: Storm, Stephen M.
ITILE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
NUMBERS OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN, DARBY & CUSHWAN
STREET: 1615 L Street, N.W.
CITY: Weahington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.4%; Score 35; DB 1; 75.0%; Pred. No. 75; tive 1; Mismatches
                                                                                                                                                                                                                                                                               Score 35; DB 1;
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/759,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REFERENCE/DOCKET NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/82732
TELECOMMUNICATION INFORMATION:
NAME: Torchia, Ph.D., A.M. REGISTRATION NUMBER: 36,700
REPERBRENCE/DOCKET NUMBER: 0NYX-005/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5481
FELEPAX: (415) 87-0663
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
MUNDER AMINO acids
MUNDER AMINO acids
MUNDER AMINO acids
MUNDER AMINO acids
                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-185-282-1; Sequence 1, Application US/08185282; Patent No. 5618670; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 648 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75...
6; Conservative
                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-151-2
                                                                                                                                                                                                                                                                                                                                                                                377 LKVVDPTP 384
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Best Local Similarity
6, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                                                                              1 LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT:
GAY Breton et. al
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AGINOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FELLING DATE: 2000-01-27
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9126
LENGTH: 405
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Patent No. 559719
GENERAL INFORMATION:
APPLICANT: Freed, Ellen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
NUMBER OF SEQUENCES:
ADDRESSEB: Cooley Godward et al.
STREET: Five Palo Alto Square
CITY: Ralo Alto
                                                                                                                                                                                 Score 35; DB 1; Length 346;
Pred. No. 37;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.4%; Score 35; DB 4; Length 405; 75.0%; Pred. No. 44; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,151
FILING DATE: 14-JUL-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9126, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                               81.4%;
  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRACMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         Unery Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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186 IKARDPTP 193
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75 LKVVDPTP 82
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US-08-276-151-5
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RESULT 14
US-08-185-282-4
; Sequence 4, Application US/08185282
; Sequence 7, Application US/08185282
; CENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.; APPLICANT: Storm, Stephen M.; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 1; Length 648; Pred. No. 75; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READSHLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RAPLICATION DATA:
APPLICATION NUMBER: US/08/185,282
                 PatentIn Release #1.0, Version #1.25
SUPERATE STATES OF STATES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/759,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REFERENCE/DOCKET NUMBER: WTS/5683/82732
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 861-3000
TELEFRAX: (202) 861-3000
TELEFRAX: (202) 862-0944
TELEFRAX: 6714627 CUSH
TELEFRAX: 6714627 CUSH
SEQUENCE CHARATTERISTICS:
LENGTH: 648 mmino acids
TYPE: amino acid
TYPE: amino acid
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.4
Best Local Similarity 75.0
Matches 6; Conservative
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377 LKVVDPTP 384
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                                                                                     Sequence 3, Application US/08185282
| Patent No. 5618670
| GENERAL INFORMATION:
| APPLICANT: Rapp, Ulf R. |
| APPLICANT: Storm, Stephen M. |
| TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES INVENES PRODESS: CORRESPONDENCES: 12
| CORRESPONDENCES: 12 |
| COUNTRY: USA |
| STREET: 1615 L Street, N.W. |
| STREET: 0.C. |
| COUNTRY: USA |
| COUNTRY: USA |
| COUNTRY: USA |
| COMPUTER: Floppy disk |
| COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.4%; Score 35; DB 1; Length 648; 75.0%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: SCOLL, WALSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/82732
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 861-3000
TELEFAX: (202) 822-0944
TELEFAX: (202) 822-0944
TELEFAX: (202) 822-0944
TELEFAX: GA14627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 anino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 LKVVDPTP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAMDPTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-185-282-3
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                                                                                                                                                                                                                                                                                            Score 35; DB 1; Length 648; Pred. No. 75; 1; Mismatches 1; Indels
                                                           Query Match 81.4%; Score 35; DB 1; Length 648; Best Local Similarity 75.0%; Pred. No. 75; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                               81.4%;
75.0%;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                          377 LKVVDPTP 384
                                    1 LKAMDPTP 8
; TOPOLOGY: linear
US-08-185-282-4
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Search completed: May 26, 2005, 19:08:41 Job time : 19.44 secs

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